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SAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                   666 SSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
20.3%; Score 767; DB 3; Length 881;
Best Local Similarity 30.1%; Pred. No. 8.1e-47;
Matches 243; Conservative 134; Mismatches 300; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNATE: F. C.
COUNTRY: US

ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FILING APPLICATION 435
PRIOR APPLICATION NUMBER: US 60/029,848
RAPLICATION NUMBER: US 60/029,848
RAPLICATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
RELEPHON, STATEM NUMBER: MA-708
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....oue Tr.
....wwkeSSE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
STATE: FL
COUNTRY: US
ZTD-TRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS: LENGTH: 881 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: 177C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                           735
                                                                                                                                                  269 IFSKKGYEIG 278
                                                                                                           726 IFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DITEFDENFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GADESVVKEAHREVINSSTEGLILINIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNI 665
                                                                                                                     WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTRPDMTLKEALKIAFGRNEP 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKANILIRDKRF 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   716
                          EKVIGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKWEDQSTQNTDSETRTISKNTSTS 300
                                                                                                                                                                               TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNL 416
                                                                                                                                                                                                                          TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNL 420
                                                                                                                                                                                                                                                                       APIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN 476
                                                                                                                                                                                                                                                                                                           421 APIALNAQDDFSSTPITMN-------YGNIATYNFENGRVRVDTGSN 460
                                                                                                                                                                                                                                                                                                                                                              WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP 536
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EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTS 296
                                                                                        RIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERIWAETMGLNTAD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09273839A
Patent No. 6329156
Patent No. 6329156
Patent No. 632916
Patent No. 632916
Patent No. 632916
APPLICANT: Carbon, Nick M
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface TITLE OF INVENTION: Receptors
FILE REFERENCE: S-89,662
CURRENT APPLICATION NUMBER: US/09/273,839A
CURRENT FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               521 NGNLOYÓGKDÍTEFDFNFDQOTSONÍKNOLAELNATNÍYTVLDKÍKLNAKANÍLÍRDKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDŢ
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33.8%; Score 1275; D
Best Local Similarity 100.0%; Pred. No. 4.4
Matches 250; Conservative 0; Mismatches
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; LENGTH: 288
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-09-273-839A-8
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US-09-273-839A-8
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209 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTINPSENGDISTNGIKKIL 268 61 94 Sequence 32, Application US/08960780

Sequence 32, Application US/08960780

Patent No. 6204435

GENERAL INFORMATION:
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schneits, James
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADPRESS:
CORRESPONDENCE ADPRESS:
CORRESPONDENCE ADPRESS: 39 QKNQ---QKEMDRKGLIGYYFKGKDF-SNLTWFAPTRDSTLIYDQQTANKLLDKKQQEYQ 4 QENRILINESESSSOGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ

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                                                                                                                                213 QKWKREIDED----TDTDGDSIPDIMEENGYTI-----QNRIAVKWDDSL-ASKGYTKFVSN 264
                                                                                                                                                                                          DSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
                                                                                                                                                                                                                                                                                              LAGERTWAETMG----LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIK 395
                                                                                                                                                                                                                                                                                                                364 VAQE--WGISIGNISQFNIASAGYLNANVRYNNVGIGAIYDVKPITSFVL-NNDIJAIII 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------LLLNID-----KDIRKILSGYIVBIEDTE------GLKE 654
95 SIRWIGLIQSKETGDFTFNLSEDEQALIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKQYSSNNPDANLTLNTDAQEKLNKARDYYISLYMKSEKNTQCEITIDGEIYPITTKTVN
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                                                                                                                                                                        PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
                                                                                                                                                                                                                                                      TIKPDMILKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                                       SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPEFNKKESQEFLAKPSKINLFT
                                                                                                          SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS
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Patent No. 6242669
GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: Feitelson, Jerald S.

APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, Brian A.

APPLICANT: Schneith E.

APPLICANT: Schneith E.

APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Stamp, Lisa
APPLICA
RESULT 11
US-09-073-898-32
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339

DSETRIISKNISISRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS

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ADENQLSQILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQV

282 320

PLESHTVGDPYTDYEKAARDLDLSNAKETFNPLVAAFPSVNVSMEKVILSPNENLS----

PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT

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RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162

SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPEFNKKESQBFLAKPSKINLFT 163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 213 QXMKREIDED----TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN

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SAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 QENRILINESESSSQGLIGYYFSDINFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
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                                                                                                                                                                                                                                                                                                                                                 Version #1.30
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20.3%; Score 767; DB 3; L
Best Local Similarity 30.1%; Pred. No. 8.1e-47;
Matches 243; Conservative 134; Mismatches 300;
41st Street, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIPTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 69/060,780
FILING DATE: 30-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAWE: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REPRENCE/DOCKET NUMBER: MA-708C1
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING PATENTIN Release #1.0, TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
                                                                           STAIL:
CCUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
PC COMPALIDLE
TANDER: IRM PC COMPALIDLE
TOWNS TYPE: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PS177C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                     Gainesville
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US-09-307-106-8

US-09-307-106-8

Sequence 8, Application US/09307106

Patent No. 6603063

GENERAL INFORMATION:

APPLICANT Fettelson, Jeraid S.

APPLICANT Schneid Eries

APPLICANT Schneid Brian A.

APPLICANT Schneid Brian Brian A.

APPLICANT Schneid Brian B
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REFERENCE/DOCKET NUMBER: MA-708C2
TELECOMOUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEPHONE: 352-375-800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PS177C8a
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SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                            481 DG---VYKIKDTHGNIVTGGEWNGVIQQIKAKTASIIVDDGE-RVAEKRVAAKDYENPED
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APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Orich J
APPLICANT: Orich J
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
APPLICANT: Estruch, Juan J
TILE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
                                       RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS--
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ADDRESSEE: CIBA-GBIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08471033
Patent No. 5770696
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US-08-471-033-5
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                                                                                                                                                                                                                                                                                                             Stamp, Lisa
Morrill, George
INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 QENRILINESESSSGGLIGYYFSDINFOAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
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20.3%; Score 767; DB 4; Length 881;
Best Local Similarity 30.1%; Pred. No. 8.1e-47;
Matches 243; Conservative 134; Mismatches 300; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-MAY-2001
CLASSIFICATION: <UNMAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/073,898

RILING DATE: 06-MAY-1998

APPLICATION NUMBER: US 08/960,780

FILING DATE: 30-0CT-1997

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INDIVIDUAL ISOLATE: PS177C8
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-850-351A-32
    764 IKQIYSRYGIKLEDGILIDKKGGIHYG 790
                                                                                                                                                                                                                                                           Loewer, David
Dullum, Charles Joseph
Muller-Cohn, Judy
                                                                                            Sequence 32, Application US/09850351A
Patent No. 6556908
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S. Schnepf, H. Ernest
Narva, Kenneth E. Stockhoff, Brian A. Schmeits, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                             -09-850-351A-32
                                                                                                                                                                                                                                                                                                                                                           LITLE OF
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651 KKQYSSNNPDANLTLMTDAQEKLNKNRDYYISLYMKSEKNTQCEITIDGEIYPITTKTVN 710
          TIKPDMILKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL-- 569
                                           ------LLENID-----KDIRKILSGYIVBIEDTE-------GLKE
                                                                                                                                                                                                                                                                                                                      655 VINDRYDMLN------ISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKE
                                                                                                             ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Warren, Gregory W
APPLICANT: Warren, Gregory W
APPLICANT: Worlel, Michael G
APPLICANT: Wallins, Marcha A
APPLICANT: Wellins, Marcha A
APPLICANT: Orar, Brian
APPLICANT: Carr, Brian
APPLICANT: Costicha, Nalini M
APPLICANT: Betruch, Juan J
APPLICANT: Betruch, Juan J
APPLICANT: Betruch, Juan J
APPLICANT: Betruch, Juan J
APPLICANT: Betruch, Juan J
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APPLICANT: Betruch
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COMPUTER READABLE FORM:
MIDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DEATH FOR COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SQLv3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541.8582
                                                                                                                                                                                                                                                                                                                                                                                                                         NTIINPSENGDT-STNGIK---KILLFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           761 N--LTDSEIKQIYSRYGİKLEDGİLİDKKGGIHYG 793
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CLASSIFICATION: 800
PRIOR PAPLICATION BATE: 800
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-UNN-1995
PRIOR PAPLICATION DATA: APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR PAPLICATION NUMBER: US 08/218,018
FILING DATE: 23-WAR-1994
PRIOR APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-WAR-1994
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-WAR-1994
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 5, Application US/08471044; Patent No. 5840868; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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20.3%; Score 765; DB 1; Length 884;
Best Local Similarity 30.1%; Pred. No. 1.1e-46;
Matches 245; Conservative 129; Mismatches 295; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SQLv3 TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8582
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-5EP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-193
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTATION NUMBER: P-40,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acids
TOPOLOGY: 1:-CLECTTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NATNIYTVLDKIKLNAKANILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKE 704
                                                                                                                                                                                                                     Query Match

20.3%; Score 765; DB 2; Length 884;
Best Local Similarity 30.1%; Pred. No. 1.1e-46;
Matches 245; Conservative 129; Mismatches 295; Indels 146; Gaps
                                                                                                                                                                                              4 QENRLINESESSSOGLIGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTIINPSENGDT-STNGIK---KILIFSKKGYEIG 735
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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 884 amino acids
; TYPE: amino acid
; TYPE: amino acid
; MOLECULE TYPE: protein
US-08-471-044-5
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Search completed: May 3, 2004, 19:42:47 Job time : 17.0986 secs Sequence 16, Appl Sequence 17, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 23, Appl Sequence 7, Appli Sequence 6, Appli Sequence 9, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli Sequence 681, Appli Sequence 681, Appli Sequence 681, Appli

Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 24, Appli Sequence 24, Appl Sequence 21, Appl Sequence 22, Appli Sequence 8, Appli Sequence 9, Appli Sequence 9, Appli Sequence 24, Appli

Sequence

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1 EVKQENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSBLENIPSENQYF 60

1 EVKQENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY

61

Sequence

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33.45 34.45 34.45

Score

Result No.

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Sequence 30, Application US/10410647

Sequence 30, Application US/10410647

Publication No. US20303235818A1

GENERAL INFORMATION:
APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: Bordner, Andrew
APPLICANT: Bordner, Andrew
APPLICANT: Bordner, Mary
ITILE OF INVENTION: IMMUNOGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME
FILE REFREENCE: PLEXUS US/10/410,647

CURRENT APPLICATION NUMBER: US 60/373,668
PRIOR APPLICATION NUMBER: US 60/373,668
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-17
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
LENGTH: 735
LENGTH: 735
LENGTH: 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 3753; DB 15; Length 735; 99.6%; Pred. No. 2.8e-274; ive 0; Mismatches 3; Indels 0
2 US-09-848-909-15
2 US-09-848-909-16
2 US-09-848-909-17
2 US-09-848-909-19
2 US-09-848-909-19
2 US-09-848-909-19
2 US-09-848-909-20
2 US-09-848-909-21
2 US-09-848-909-21
3 US-10-442-502-6
5 US-10-442-502-6
5 US-10-442-502-6
6 US-10-442-502-6
7 US-10-442-502-7
7 US-10-442-502-7
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Matches 732; Conservative
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| cgn2_6/ptodate/2/pubpaa/PCT_RW PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/PCT_RW PUB.pep:*
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| cgn2_6/ptodate/2/pubpaa/USO6_NBW PUB.pep:*
| cgn2_6/ptodate/2/pubpaa/USO7_NBW PUB.pep:*
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| cgn2_6/ptodate/2/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodate/2/pubpaa/USO9_PUBCOMB.pep:*
| cgn2_6/ptodate/2/pubpaa/USO0_PUBCOMB.pep:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Minimum DB Maximum DB

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Perfect score: Scoring table:

Run on:

Sequence:

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US-09-84-909-2
; Sequence 2, Application US/09848909
; Publication No. US20020039588A1
; GENERAL INFORMATION:
    APPLICANT: Collier, R. John
; APPLICANT: Collier, R. John
; TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: Compounds
; TITLE OF INVENTION: Compounds
; TITLE OF INVENTION: COMPOUNDER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR PILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                               ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                                                    DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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US-09-848-909-1
US-09-848-909-1
Sequence 1, Application US/09848909
Publication No. US20020039588A1
SCHEAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Seniman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: 20000000
CURRENT FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
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Pred. No. 2.9e-274;
0; Mismatches 3;
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SOFTWARE: FASUSEQ for Windows Version
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LENGTH: 736
TYPE: PRT
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APPLICANT: Coller, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
                       Length
                                               Indels
                      Score 3753; DB 12;
Pred, No. 2.9e-274;
0; Mismatches 3;
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                       99.5%;
                     Query Match
Best Local Similarity 99.6
Matches 732; Conservative
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0
                                                           Length 736;
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APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
                                                                                                Indels
                                                       Score 3753; DB 12;
Pred. No. 2.9e-274;
0; Mismatches 3;
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Publication No. US20020039588A1
GENERAL INFORMATION:
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; ORGANISM: Bacillus anthracis
US-09-848-909-3
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                                                         Query Match
Best Local Similarity 99.6
Matches 732; Conservative
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TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/060002
CURRENT PEPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENTH: 736 ; TYPE: PRT ; ORGANISM: Bacillus anthracis US-09-848-909-4

UB-UY-848-YUYA-IS. TADD

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Gaps ., Length 736; Indels Query Match 99.5%; Score 3753; DB 12; Best Local Similarity 99.6%; Pred. No. 2.9e-274; Matches 732; Conservative 0; Mismatches 3;

120 9 EVKQENKLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 1 BVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY Н 61

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GRIDKOVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKOVTSTSRTHT 300 NNIAVGADESVVXEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR DMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHBKKGLTKYKSSPEKWSTASDPYSDFEKVT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 1 BVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL LNAOKDASSTPITMNYNOFLELEKTKOLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL NNIAVGADESVVKEAHREVINSSTEGLILNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF ô Sequence 5, Application US/09848909
Publication No. US20020039588A1
GENERAL INPORMATION:
TERMINAT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
FRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastERO for Windows Version 4.0
FACILIES OF SECULO FOR WINDOWS WINDOWS WESTON 100 S Length 736; 99.5%; Score 3753; DB 12; 99.6%; Pred. No. 2.9e-274; live 0; Mismatches 3; IKKILIFSKKGYEIG 735 TYPE: PRT CRGANISM: Bacillus anthracis US-09-848-909-5 Query Match Best Local Similarity 99.6' Matches 732; Conservative 421 541 601 181 361 421 541 601 199 661 721 481 61 241 241 301 301 q g ò g ઠે d ò 셤 ò d ò 엄 ò 임 ò ద δ g ò 유 ò d ð ò ð

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                                                                               Sequence 6, Application US/09848909; Sequence 6, Application US/09848909; Publication No. US2020039588A1; GENERAL INFORMATION:
APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; TITLE OF INVENTION: Compounds and Methods for the Treatment; TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection; FILE REFERENCE: 00742/060002; CURRENT APPLICATION NUMBER: US/09/848,909; CURRENT APPLICATION NUMBER: US/09/848,909; PRIOR FILING DATE: 2000-04-04; NUMBER OF SEQ ID NOS: 35; SCFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6
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99.5%; Score 3753; DB 12;
Best Local Similarity 99.6%; Pred. No. 2.9e-274;
Matches 732; Conservative 0; Mismatches 3;
                 735
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; ORGANISM: Bacillus anthracis
US-09-848-909-6
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| Publication No. US20020039588A1
| Publication No. US20020039588A1
| APPLICANT: Collier, R. John
| APPLICANT: Callman, Brett R.
| TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | URRENT APPLICATION NUMBER: US/09/0448,909 | CURRENT FILING DATE: 2000-04-04 | NUMBER OF SEQ ID NOS: 35 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 7 | LENGTH: 736 | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: RRI | TYPE: Length 736; 4 L4:31:00 Z004

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US-09-848-909-8
Sequence 8, Application US/09848909
; Publication No. US20020039588A1
; Publication No. US20020039588A1
; APPLICANT: Collier, R. John
; APPLICANT: Collier, R. John
; TILE OF INVENTION: Compounds and Methods for the Treatment
; TILE OF INVENTION: and Prevention of Bacterial Infection
; TILE REPRENCE: 00742/06002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; TOWN OR SEQ ID NOS: 35
; SOFTWARE: PASTSEQ for Windows Version 4.0 Length 736; Indels Query Match 99.5%; Score 3753; DB 12; Best Local Similarity 99.6%; Pred. No. 2.9e-274; Matches 732; Conservative 0; Mismatches 3; IKKILIFSKKGYEIG 735 IKKILIFSKKGYEIG 735 TYPE: PRT CRGANISM: Bacillus anthracis US-09-848-909-8 LENGTH: 736 181 361 61 121 181 241 421 601 661 661 721 721 121 301 301 361 541 601 8 g δ 8 엄 $\dot{\circ}$ g g à d ò DD δ g à g Db δ 8 8 Db

120 61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120 240 240 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 300 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300 720 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 540 540 900 900 9 99 SEVHONAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 360 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA 420 09 9 601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPWVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY LPQIQETTARIIPNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMYLLIRDKRFHYDR 601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF ô RESULT 10
US-09-848-909-9
Sequence 9, Application US/09948909
Sequence 9, Application US/09948909
Publication No. UB20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REFERENCE: 0742/066002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR PELING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 736 Length 736; Indels Query Match 99.5%; Score 3753; DB 12; Best Local Similarity 99.6%; Pred. No. 2.9e-274; Matches 732; Conservative 0; Mismatches 3; 721 IKKILIFSKKGYEIG 735 721 IKKILIFSKKGYEIG 735 TYPE: PRT; ORGANISM: Bacillus anthracis US-09-848-909-9

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US-09-848-909-11
Sequence 11, Application US/09848909
Sequence 11, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
FILE REPERBNCE: 0742/060002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 736
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CRGANISM: Bacillus anthracis
US-09-848-909-11
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US-09-848-909-10
Sequence 10, Application US/09848909
Sequence 10, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
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TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: 2014/060002
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
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Pred. No. 2.9e-274;
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Best Local Similarity 99.6%;
Matches 732; Conservative
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                                          QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSKKRSTSAGPTVPDRDN
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Sequence 13, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds
TITLE OF INVENTION: Compounds
CURRENT FILING DATE: 2001-08-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PSECEEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 736
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Pred. No. 2.9e-274;
); Mismatches 3; Indels 0
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Matches 732; Conservative (
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APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/06002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
NUMBER: OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 736
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Pred. No. 2.9e-274;
0; Mismatches 3;
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Publication No. US20020039588A1
GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 732; Conservative
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US-09-848-909-12
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US-09-848-909-12
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                                       QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                               61 OSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                         QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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RESULT 12
USS-09-848-909-14

Sequence 14, Application US/09848909

Publication No. US2020039588A1

GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
TITLE OF INVENTION: 10742/06002
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800

PRIOR PILING DATE: 2000-04-04

NUMBER OF FELLO ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO. 14

LENGTH: 736

TYPE: PRT

ORGANISM: Bacillus anthracis
US-09-848-909-14
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                                                 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                          Gaps
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   Length 736;
                          Indels
Score 3753; DB 12;
Pred. No. 2.9e-274;
0; Mismatches 3;
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   Query Match
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May 3, 2004, 19:36:13 ; Search time 175.546 Seconds (without alignments) 4086.665 Million cell updates/sec US-09-848-909A-13 3772 1 EVKQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG Total number of hits satisfying chosen parameters: 6019581 seqs, 976053577 residues first 45 summaries protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Post-processing: Minimum Match 0% Maximum Match 100% Minimum DB seq length: 0 Maximum DB seq length: 200000000 Scoring table: score: • OM protein Sequence: Searched: Database Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ARIES

Result Query No. Score Match Length DB ID

Description

1 3772 100.0 735 1 PCT-USO3-35733-13 Sequence 13, Appl 2 766 99.8 755 2 105-09-648-0904-13 Sequence 13, Appl 2 766 99.8 755 12 PCT-USO3-35733-2 Sequence 2, Appl 2 766 99.8 755 12 PCT-USO3-3573-2 Sequence 2, Appl 2 766 99.7 735 1 PCT-USO3-3573-5 Sequence 2, Appl 2 769 99.7 735 1 PCT-USO3-3573-9 Sequence 2, Appl 1 755 99.7 735 1 PCT-USO3-3573-9 Sequence 2, Appl 1 755 99.7 735 1 PCT-USO3-3573-9 Sequence 2, Appl 1 755 99.7 735 1 PCT-USO3-3573-9 Sequence 3, Appl 1 755 99.7 735 1 PCT-USO3-3573-9 Sequence 3, Appl 1 755 99.7 735 1 PCT-USO3-3573-6 Sequence 3, Appl 1 755 99.7 735 1 PCT-USO3-3573-4 Sequence 3, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 2, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 3, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 2, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 3, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 4, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 7, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-4 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-1 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-1 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-1 Sequence 2, Appl 1 755 99.5 735 1 PCT-USO3-3573-1 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-1 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 755 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 752 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 1, Appl 1 753 99.5 735 1 PCT-USO3-3573-2 Sequence 2, Appl 1 775 99.5 735 1 PCT-USO3-3573-2 Sequence 2, Appl 1 775 99.5 735 1 PCT-USO3-3573-2 Sequence 2, Appl 1 775 99.5 775 1 PCT-USO3-3573-2 S

LIGNMENT

PCT-US03-35733-13

Sequence 13, Application PC/TUS0335733

Sequence 13, Application PC/TUS0335733

Sequence 13, Application of Bacterial Infection ITLE OF INVENTION: Compounds and Methods for the Treatment ITLE OF INVENTION: and Prevention of Bacterial Infection FILE OF INVENTION: MUBBER: PCT/US03/35733

CURRENT APPLICATION NUMBER: PCT/US03/35733

CURRENT FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FattSEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 735

TYPE: PRT

ORGANISM: Bacillus anthracis

Query Match

100.0%; Score 3772; DB 1; Length 735;

Best Local Similarity 100.0%; Pred. No. 1.86-298;

Matches 735; Conservative 0; Mismatches 0; Indels 0,

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Gaps

US-09-848-909A-13

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Length Indels 1 EVKQENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

RESULT 2
US-00-840-13
US-00-840-13
US-00-840-13
US-00-840-13
Sequence 13, Application US/09848909A
Sequence 13, Application US/09848909A
SEXERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TILLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060025
CURRENT FILING DATE: 2000-05-04
CURRENT PRILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
NUMBER: OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 735
TYPE: PRI
CREANISM: Bacillus anthracis

300 720 120 180 180 240 240 300 480 540 540 900 900 999 999 720 120 360 360 420 420 480 9 481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGI PDSLEVEGYTVDVKNKRTFLSPWI SNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFPDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQ1LAPNNYYPSKNLAPIA INAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKBALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIBDTEGLKEVINDRY NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG EVKQENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL OSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY RESULT 3
PCT-USO-35733-10
Sequence 10, Application PC/TUSO335733
Sequence 10, Application PC/TUSO335733
GENERAL INFORMATION:
TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/USO3/35733
CURRENT FILING DATE: 2003-110-10
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2003-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PRACESEQ for Windows Version 4.0 721 IXKILIFSKKGYEIG 735 721 IXKILIFSKKGYEIG 735 601 1 241 421 601 661 Н 61 121 121 181 181 301 301 361 361 421 541 541 g ò g

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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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US-09-848-909A-10
                                                                                                    TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Collier, T. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Pervention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
                                                                                                                  Indels
                                                                                      Score 3766; DB 1;
Pred. No. 5.5e-298;
0; Mismatches 1;
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Matches 734; Conservative
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LENGTH: 735
TYPE: PRT
CORGANISM: Bacillus a
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   Length 735;
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Score 3766; DB 23;
Pred. No. 5.5e-298;
0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
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   99.8%;
   Query Match
Best Local Similarity 99.9'
Matches 734; Conservative
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Sequence 2. Application PC/TUS0335733
; GENERAL INPORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFRENCE: 00742/072003
; CURRENT APPLICATION NUMBER: PCT/US03/35733
; CURRENT FILING DATE: 2003-10-10
PRIOR PILING DATE: 2003-10-10
; PRIOR PILING DATE: 2003-11-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; FEWINE OF SEX DATE: 2004-11-08
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.7e-297;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 733; Conservative (
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PCT-US03-35733-2
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   TITLE OF INVENTION: Modified Shine Dalgarno Sequences and Methods of FILE REFERENCE: PV595PCT
CURRENT APPLICATION NUMBER: PCT/US03/19786
CURRENT APPLICATION NUMBER: PCT/US03/19786
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 735
TYPE: PRT
CRAMISM: Artificial sequence
                                                                                                                                                                                                                                                        Length 735;
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Pred. No. 9.7e-298;
1; Mismatches 1;
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RESULT 6 PCT-US03-35733-2

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Sequence 8, Application PC/TUS0335733

GENERAL INFORMATION:

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE REPRENCE: 0.0742/072003

CURRENT FILING DATE: 2003-10-10

PRIOR FILING DATE: 2003-10-10

PRIOR FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 735
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Pred. No. 2.1e-297;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 733; Conservative
                                                                          ikkiliFskkGYEIG 735
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; ORGANISM: Bacillus anthracis
PCT-US03-35733-8
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                                                   VESCUL, (SERVEL) Application US/09848909A

Sequence 2, Application US/09848909A

Sequence 2, Application US/09848909A

SEGNERAL INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Collier, R. John

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: and Prevention of Bacterial Infection

FILE REFERENCE: 0742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT PILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 735
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.larity 99.7%; Pred. No. 1.7e-297;
Conservative 0; Mismatches 2;
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Matches 733; Conserv
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APPLICANT: Collier, R. John
TILE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT FILING DATE: 2001-05-04
PRIOR PILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Pred. No. 2.1e-297;
); Mismatches 2;
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US-09-848-909A-8
Sequence 8, Application US/09848909A
; GENERAL INFORMATION:
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Best Local Similarity 99.7%;
Matches 733; Conservative (
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APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REPERRICE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: US 60/424,987
PRIOR PFLING DATE: 2003-10-10
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 735
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Pred. No. 2.1e-297;
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Best Local Similarity 99.7%;
Matches 733; Conservative
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180 999 720 61 OSAIWSGFIKVKKSDEYTFATSADNHVTMMVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120 120 121 QRENPIEKCLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 240 240 540 540 600 900 99 480 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKATSTSRTHT 300 360 9 9 541 QYQCKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKANILIRDKRFHYDR DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKAVEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL SEVHGNAEVHASFFDI GGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 1 EVKOENRILINESESSSOGLIGYYFSDINFOAPMVVTSSTTGDLSIPSSELENIPSENOYF 1 EVKQENRLINESESSSQGLLGYYPSDLNFQAPWVVTSSTTGDLSIPSSELENIPSENQYF QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVKKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIARGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR LNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LNAQDDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV .. 0 Gequence 7, Application PC/TUS0335733

Gequence 7, Application PC/TUS0335733

GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
ITLE OF INVENTION: Compounds and Methods for the Treatment
ITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003

CURRENT APPLICATION NUMBER: PCT/US03/35733

CURRENT FILING DATE: 2002-11-09

PRIOR PILING DATE: 2002-11-09

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 735 Length 735; Indels Score 3755; DB 1; Pred. No. 4.4e-297; 1; Mismatches 2; 721 IKKILIFSKKGYEIG 735 Query Match
Best Local Similarity 99.6%;
Matches 732; Conservative 735 ORGANISM: Bacillus anthracis PCT-US03-35733-7 IKKILIFSKKGYEIG RESULT 12 PCT-US03-35733-7 421 481 541 601 601 661 661 721 61 121 181 181 241 241 301 301 421 TYPE: PRT PP g g g õ g g g à ò q ठे g ò à à ò ò ò g ò 120 240 240 660 960 720 120 300 420 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA 420 9 9 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 661 DMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQ1LAPNNYYPSKNLAPIA QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG EVKQENRILNESESSSQGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 1 EVKOENRLINESESSSOGLIGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL Gaps ö Sequence 9, Application US/09848909A; Sequence 9, Application US/09848909A; GENERAL INFORMATION:

APPLICANT: Collier, R. John
APPLICANT: Collier, B. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT FILING DATE: 2001-05-04
PRIOR PILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 735 Length 735; Indels Score 3759; DB 23; Pred. No. 2.1e-297; 0; Mismatches 2; Query Match
Best Local Similarity 99.7%;
Matches 733; Conservative 721 IKKILIFSKKGYEIG 735 ; TYPE: PRT ; ORGANISM: Bacillus anthracis US-09-848-909A-9 RESULT 11 US-09-848-909A-9 721 61 61 121 181 181 241 301 361 361 241 301 541 661 481

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                      361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNYYPSKNLAPIA
                                                      LNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
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LOCATION: 427
COTHER INFORMATION: Xaa = any amino acid except Phe PCT-US03-35733-23
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99.6%; Pred. No. 4.4e-297;
live 0; Mismatches 3;
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Best Local Similarity 99.64
Matches 732; Conservative
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481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL

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721 IKKILIFSKKGYBIG 735

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GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT

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GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT

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Sequence 7, Application US/09848909A;
GENERAL INFORMATION:
APPLICANT: COllier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
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TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION NUMBER: US/09/848,909A;
CURRENT APPLICATION NUMBER: US 60/201,800;
PRIOR FILING DATE: 2000-05-04;
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0;
SEQ ID NO 7;
TENNING: DATE: TOWN NUMBER: US/09/840;
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721 IKKILIFSKKGYEIG 735
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CRGANISM: Bacillus anthracis
US-09-848-909A-7
                                                                                                                                                                                                                       RESULT 14
US-09-848-909A-7
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                     181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                    GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                   GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                       SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
                                                                                                                                                                                                              NANIRYVNIGTAPIXNVLPITSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA
                                                                                                                                                                                                                                                                                     INAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
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99.6%; Pred. No. 4.4e-297;
ive 0; Mismatches 3; Indels 0
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GENERAL INFORMATION:
APPLICANT: COlliar, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: And Prevention of Bacterial Infection
FILE REFERRNCE: 00742/060002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          = any amino acid except Phe
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Best Local Similarity 99.63
Matches 732; Conservative
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; OTHER INFORMATION: Xaa
US-09-848-909A-23
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LOCATION: 427
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EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

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EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 3, 2004, 19:30:47; Search time 13.0855 Seconds (without alignments) 5403.004 Million cell updates/sec

US-09-848-909A-13 3772 1 EVRQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 735 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	protective antigen		cryptic protein -			w	toxin-like outer m	membrane nuclease,	major merozoite su	Ψ	surface-located me	rhoptry protein -	hypothetical prote	botulinum neurotox	uncharacterized pr	hemolysin [importe		hypothetical prote		lmp1 protein - Myc	t organe	filamentous hemagg	probable nuclear p	able memb	urface	6	etical	hypothetical prote	Н
SOMMAKLES	QI	3993	140862	I39933	G59104	F82885	T28676	B64635	E90598	205603	B89921	JC6009	T28677	A86827	\$68218	C97033	A10452	H71879	T31105	G90599	T30822	T18372	T31102	T41023	E71622	B71704		55	F82884	6708
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de	Query	9 .		6.2	•				•	4.	4.	4.8	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5
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probable coiled-co alpha-toxin - Clos	surrace memorane p trse-like protein TyB protein - yeas	botulinum neurotox hypothetical prote	TyB protein - yeas hypothetical prote	serine proteinase hypothetical coile P115 protein - Myc	hypothetical prote hypothetical prote actin-interacting
T41342 S55805	PC6003 G90559 S52611	S11455 T18469	531282 556894 T18427	F89870 T38077 JQ0894	C90593 C90538 T37715
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ALIGNMENTS

 RESULT 1 139934 protective antigen precursor - Bacillus anthracis plasmid C;Species: Bacillus anthracis C;Date: 19-Jul-1996 #sequence revision 19-Jul-1996 #text_change 01-Dec-2000 C;Accession: 139934; S69160; F59104 R;Welkos, S;L:; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J. Gene 69, 287-300, 1988 A;Pitle: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthr A;Reference number: 139933, MUID:89172073; PMID:3148491 A;Accession: 139934 A. Accession: 139934
 A; Molecule Lype: DNA A; Residues: 1-764 < RES> A; Residues: 1-764 < RES> A; Cross-references: GB: M22589; NID: g143280; FIDN: AAA22637.1; PID: g143282 A; Cross-references: GB: M22589; NID: g143280; FIDN: AAA22637.1; PID: g143282 R; Friedman, T.C.; Gordon, V.M.; Leppla, S.H.; Klimpel, K.R.; Birch, N.P.; Loh, Y.P. Arch. Biochem. Biophys. 316, 5-13, 1995 A; Title: In vitro processing of anthrax toxin protective antigen by recombinant PC1 (SF A; Reference number: S69160; MUID: 95142670; PMID: 7840657
 A, Wolecule type: protein A, Wolecule type: protein A, Residues: 197-202 < RT. R, Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle J. Bacteriol. 181, 6509-6515, 1999 A, Title: Sequence and organization of pxOl, the large Bacillus anthracis plasmid harbor A, Reference number: A59091; MUID:99445483; PMID:10515943 A, Accession: F59104 A, Statues preliminary A, Molecule type: DNA
 A, Residues: 1-313, 'Q',315-764 <oki> A, Residues: 1-313, 'Q',315-764 <oki> A, Crosa-references: GB, AF0655404, NID: 94894216; PIDN: AAD32414.1; PID: 94894326 A, Bxperimental source: strain Sterne A, Note: similar to anthrax toxin moiety, protective antigen, pagA formerly pag, plasmic C, Genetics: A, Generics: A, Generics: A, Generics: A, Generics: A, Generics: Page A, Generics: A, Generics: Plasmid</oki></oki>
 C.Function: three component exotoxin, protective antigen binds to receptors on the sy active components edema factor or lethal factor; the complex is internalized by recef C.Reywords: exotoxin F.1-29/Domain: signal sequence #status predicted <sig>F;30-196/Domain: propeptide #status predicted <pro>F;30-196/Domain: propeptide #status predicted <pro>F;30-202/Product: protective antigen #status experimental <wat></wat></pro></pro></sig>
 Query Match 99.5%; Score 3753; DB 2; Length 764; Best Local Similarity 99.6%; Pred. No. 1.5e-182; Indels 0; Gaps 0; Matches 732; Conservative 0; Mismatches 3; Indels 0; Gaps 0; Qy 1 EVKOBIRILINESESSSQCLIGYYFSDINFQAPMVTSSTTGDLSIPSSELENIPSENQYF 60 0 0; 0; 0; 0; Db 30 EVKQENRILINESESSSQCLIGYYFSDINFQAPMVTSSTTGDLSIPSSELENIPSENQYF 89 0;

May

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Thoptry protein - Plasmodium yoelii (fragment)
C;Species: Plasmodium yoelii (fragment)
C;Species: Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Species: Plasmodium yoelii
C;Date: 12-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T226676; A45521
R;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Blochem. Parasitol. 76, 329-332, 1996
A;Title: Comparison of two members of a multigene family coding for high-molecular mass A;Reference number: Z20507; MUID:97077455; PMID:8920022
A;Accession: T22676
A;Accession: T22676
A;Accession: L2201 csnnshated from GB/EMBL/DDBJ
A;Recule type: DNA
A;Residues: 1-2401 csnn>
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                                                                                                                                                                                                     139 SQNKKEVISSDNLQLPELKQKSSN----SRKKRSTSAGPTVPDRD-------
                                                                                                                                                                                                                                                                                  ----NDGI PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSD
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    Mismatches 325;
    Conservative 131;
    Matches 174;
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G59104
hypothetical protein pXO1-111 - Bacillus anthracis virulence plasmid pXO1
C;Species: Bacillus anthracis
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C;Accession: G59104
R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
U. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori
A;Reference number: A59091; MUID:99445483; PMID:10515943
A;Accession: G59104
A;Accession: G59104
A;Accession: G59104
A;Accession: L204 coKI>
A;Molecule type: DNA
A;Residues: 1-204 coKI>
A;Residues: 1-204 coKI>
A;Residues: 1-204 coKI>
A;Residues: 1-204 coKI>
A;Residues: 1-204 coKI>
A;Gcrez-references: GB:AF065404; NID:94894216; PIDN:AAD32415.1; PID:94894327
A;Experimental source: strain Sterne
C;Genetics: A;Gene: pXO1-111
A;Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Figures: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Accesion: F82885
R;Glass, J.I.; LekKowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
S;Glass, J.I.; LekKowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
S;Dascription: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82875
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-4688 < GLA>
A;Residues: 1-4688 < GLA>
A;Cross-references: GB:AE022145; GB:AF222894; NID:g6899476; PIDN:AAF30894.1; GSPDB:GN001
C;Genetics:
A;Genetics: A;Genetic code: SGC3
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    646
                                                                           647 EDTE------GLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPN 693
                                                                                                    647 EDTE------GLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPN 693
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                       MNILIRDKR FHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI
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                                                                                                                                                          694 YKVNVYAVIKEN-TIINPSENGDISINGIKKILIFSKKGYEI 734
                                                                                                                                                                                    Query Match 6.2%; Score 235.5; DB 2; Best Local Similarity 34.6%; Pred. No. 2.6e-05; Matches 56; Conservative 36; Mismatches 47;
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No. 0.13;
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A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
R;Keen, U.; Holder, A.; Playfair, U.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 4-44; 1990.
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple
A;Reference number: A45521; MUD:91101660; PMID:2270106
A;Accession: A45521
A;Status: preliminary
A;Mostatus: 2260-2401 < KEE>
A;Cross-references: GB:M34281

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Indels 221; Length 2401; Query Match 5.1%; Score 190.5; DB 2; Best Local Similarity 21.7%; Pred. No. 0.19; Matches 182; Conservative 119; Mismatches 316;

461 46 PSSELENIPSENQYFQSAI--WSGFIKV---KKSDEYTFAISADNHVTMWVDDQEV---I 97 ---FOAPMVVTSSTTGDLSI 1 EVKOENRLINESESSSOGLLGYYFSDLN------8 & 8 8 g ò ò

NKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELK 98

QKSSNSRK--KRSTSAGPTVPDRDNDGIPD-----SLEVEGYTVDVKNKRTFLSP 158

MENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS 266 678

-----KVKANVT NSNSSTVAI - DHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLV 714 326

TVLDKIKLNAKMNILIRDKRF--HYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDK 633 PDMTLKEALKIAFGFNEP---NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIY ISDIRKNSLKIIQDFSEESYINDIKKELEKNVLE----SQNNNTDINQYLSKIE--NIY 932

> δ 음 강

--EXI----ITQLKENSSLKECQSKIKSTIDDNYVSECIKNITNL----KTYIVNEKNN- 1069 DIRKILSGYIVEIEDTEGLKE-----VINDRY---DMLNISSLRQDGKTFIDFKKYND 683 634

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Cipecies: Helicobacter pylori Cipecies: Helicobacter pylori Cipecies: Helicobacter pylori Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 Cipate: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 Cipate: 06-Oct-1999 Cipate:

43;

239; Length 2529; Indels Query Match 5.0%; Score 189.5; DB 2; Best Local Similarity 21.0%; Pred. No. 0.23; Matches 158; Conservative 92; Mismatches 264;

ENPTEKGLDFKLYWTDSQNK----KEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDR 123 729

---GRSFSVNIQNGTLIIGNNTESVNSNGLIMIGHGGFGYITGTFSAANIY----LTNNF DNDGIPDSLEVEGYTVDVKNYRTFLSP----WI-----SNIHEKKGLTKYK 179

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322 SSPEKWST------ASD----PYSDFEKVTGRIDKNVSPEARHPLVAAYPIV HVDMBNIILSKNEDOSTONTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSA KTGEGVSNSDGGGANITFKASDNITMDGLNYNDAETVTKMIQTGAS---QHSYATFDALN 221 833 263 qq 8 g &

890

325

-----PITSLVLGKNOTLATIKADENQLSQILAPNNYYPSKNLAPIAL-NAQKDASS 429 GFTNPGGSSVISANATNSLSFINSR-----LNGGAVYNLQANSLIFN-NTQAVFNVLY GPSNSNSSTVA---IDHSLSLAGERIWAETMGLNTADTARLNANIRYVNTGTAPIYNVL-323 922 379

8 & 8

.026 NSLTLDNNSNLSLDNQSVLNANNTSAFNNQASLNIYNGS------QATEN 1069 TPITMMYNQFLELEKTKOLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTA 489 SRGTSNFNATTQLLGNTNFTLSS-----QSLLNFNGDTTLQNNANITLGNKSQAAFK 974 430

1127 DFGGNTIIDTASFNFDSASSLNFNNLTANGALNFNGYTPSLTKALMSVSGQFVLGNNGDI EF----DFNFDQQTSQNIKNOLA---

----HYDRNNIAVG 570 NATHIYTVLDKIKLNAKMNILIRDKRF------

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| SDNQA----GTYYLTSNIKGLFTPKGSQTPQAPGTYSPFNQPLSSLNIYNKGFSSENLK 1360 607 A-----DESVVKEAHR-----EVIN--SSTEGLLLNIDKDI------RKILSGYIVEI EDTEGLKEVINDRYDMLNISSL------RODGKTFIDFKKYNDKLPLY---ISNPNYK

TLLGILSQNSATLKEMIESNQLDNITN-INEVL 1392 VNVYAVTKENTIIN ---PSENGDTSTNGIKKIL 9 δ

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TSTNGIKKI-----LIFSKKG 731
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                                                                 Describes muclease, lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C,Species: Mycoplasma pulmonis
C,Species: Mycoplasma pulmonis
C,Accession: E9058
R,Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Mucleic Acids Res. 29, 2145-2133, 2001
A;fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MulD;21267165; PMID:11353084
A,Accession: B90598
A,Accession: B90598
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 17-1125 «KUR»
A,Molecule type: DNA
A,Esciences: GB:AL445566; PID:g14090108; PIDN:CAC13866.1; GSPDB:GN00153
A;Schrimental source: strain UAB CTIP
A;Genetic code: SGG3
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Best Local Similarity 19.1%; Pred. No. 0.1;
Matches 165; Conservative 162; Mismatches 330;
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Major merozoite surface antigen precursor - malaria parasite (Plasmodium falcipa major merozoite surface antigen

C,5geciese: Plasmodium falciparum

C,3geciese: Plasmodium falciparum

C,Accession: S05603 #sequence_revision 12-Peb-1993 #text_change 09-Jun-2000

C,Accession: S05603 #sequence_revision 12-Peb-1993 #text_change 09-Jun-2000

C,Accession: S05603 #sequence_revision 12-Peb-1993 #text_change 09-Jun-2000

R,Myler, P.J.

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Nucleic Acids Res. 17, 5401, 1989

A,Title: Nucleoctide and deduced amino acid sequence of the gp195 (MSA-1) gene fr

R,Myler, P.J.

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BSGSDTLEQSQPKKPASTHVGAES---NTITTSQ-NVDDEVDDVIIVPIFGESREDYDDL 1256
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                                                             ---LNIDKDIRKILSGYIVEIEDTEGLKEVINDR
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                                                                                                                                                                                YDMLNISSLRQDGKTF-IDFKKYNDKLFLYISNPNYKVNVYAVTKENT-
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Best Local Similarity 20.5%; Pred. No. 0.22;
Matches 170; Conservative 138; Mismatches 256;
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286 TRII 2720 LATAKQ		Qy 383LVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALNAQKDAS 428	429	QY 460 ATYNFENGRVRVDTGSNWSEVLPQIQE-TTARIIFNGKDLNLVERRIAAVNPS 511	512 DPLET		600 RNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVIN 	Qy 658 DR	K.; Qy 709 NPSEN 713	Db 3192 DQTTN 3196	RESULT 11 JC6009 surface-located membrane protein lmp3 precursor - Mycoplasma hominis	C.Species: Mycopiasma nominis C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000 C.Accession: JC6009 R.Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.	J Bacteriol. 178, 2775-2784, 1996 A;Title: Analygis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene sys A;Teference number: JC6009; MUID:96213016; PMID:8631664 A;Accession: JC6009	A; Molecule type: DNA A; Residues: 1-1302 <lad> A; Creating : references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336</lad>	A) General Imp3 A) Gener: Imp3 A) Generic code: SGC3 A) Answerfamily any factor located membrane protein lmp3; tetratricopeptide repeat homology	equence #status predicted <sig></sig>	ips #scatco predictor TT1> <tt2> <tt3></tt3></tt2>	F;1154-1190/Domain: tetratricopeptide repeat homology <tt4> Query Match Conery Match</tt4>	ST DOCAL SIMILATILY 1777, 1700 COHES 137; CONSELVATIVE 141; M
OY 382 -SLVLGKNOTLATIKADENQLSQLLAPNNYYPSKNLAPIALNAQKDASSTPITMNYN 437	VKDILNSRFNKRENFKNV-LESDLIPYKDLTSSNYVVKDPYKFLNKEKRDKFLSSYNYIK	482 PQIQETTARIIENGKDLNLVERRIAAVNPSDPLETTKPUM-TLKBALKLAFGF >3.3 	534 NEPNGNLQYQGKDITE	577 VLDKIKLNAKONILIRDKREHYDRNNIAVG-ADESVVKEAHREVINSSTEGLL 628 : :	QY 629 LNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLP 686	Oy 687 LYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKI 724 :	RESULT 10 89921 hypothetical protein ebhA [imported] - Staphylococcus aureus (strain N315)	Species: Staphylococcus aureus Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 Accession: B89921	<pre>kuroda, m.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cul, b.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, .; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.</pre>	ncet 357, 1225-1240, 2001 Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. Reference number: A89758; MIDD:21311952; PMID:11418146	A,Accession: B89921 A,Status: preliminary A,Molecule type: DNA A,Residues: 1-6713 «KUR»	<pre>Lross-references: GB:BA000018; PID:gl3701232; PIDN:BAB42527.1; GSPDB:GN00149 Sxperimental source: strain N315 aenetics:</pre>	Gene: ebruk Query Match Best Local Similarity 20.4%; Pred. No. 2.1; 21; 22; Indels 256; Gaps 43; Matches 172; Conservative 125; Mismatches 292; Indels 256; Gaps 43;	9 INESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSENQYFQSA 6	Db 2468 VRQAKSDAKANLG-TLTHINNAQKQDLTSQIEGATTVNGVNSVKIRAQULDGAMQKLHSA 2520 Qy 64 IWSGFIKVKKSDEYTPATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKI 118	2527	QY 119 QYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGP 173	QY 174 TVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEK 225	226 WSTASDPYSDFEKV : : : : 2673 QGAYTDAYNAAKNI

35;

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701 169 752 224 807

643

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hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: A86827 R;Solotin, A:; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001
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                                                                                                                                                                                                                      EVANIYNI-LKLNKIKKIIDKVKEYTSEIEKNKK------NINDELNNSEKVIKKI
                                                                                                                                       Gaps
                                                                                    4.8%; Score 181; DB 2; Length 2269;
ilarity 20.5%; Pred. No. 0.53;
Conservative 121; Mismatches 301; Indels 204;
A,Molecule type: DNA
A,Residues: 2131-2269 <KE2>
A,Cross-references: GB:M34283
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       QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGR--LYQIKI 118
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C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
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botulinum neurotoxin type A, nontoxic/nonhemagglutinating - Clostridium botulinum (stra c) Species: Clostridium botulinum
A,Variety: strain NIH
A,Variety: strain NIH
C,Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 02-Jun-2003
C,Accession: S68218; S74301
R,Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
FBBS Lett. 376, 41-44, 1955
A,Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin component A,Reference number: S67988; MUID:96096783; PMID:8521962
A,Accession: S68218
A,Molecule type: DNA
A,Residues: 1-1193 *FUJ>
A,Residues: 1-1193 *FUJ>
A,Residues: 1-1193 *FUJ>
A,Residues: 1-1193 *FUJ>
A,Residues: 1-1193 *FUJ>
A,Residues: 1-13,145-155 *FUJ>
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F;1-1193/Product: botulinum neurotoxin type A, nontoxic/nonhemagglutinating #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: tetanus toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLYW----
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Best Local Simi
Matches 181;
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s6
A;Reference number: A86625; MUD:21235186; PMID:11337471
A;Accession: A86625
A;Atatus: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1072 < STO>
A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146
C;Genetics: A;Gene: yqfG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TNILPPSNPTESNSVSDOTSSEASTNSNSSISLSPSNISSTSDSESATNSSDFSNVAEVA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R----LEKGRLYQIKIQYQRENPTEKGLDFKL----YWTDSQNKKEVISSDNLQLPELK 157
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                                                                                                                                                                                                                                                                                                                                                                 197;
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                                                                                                                                                                                                                                                                                                       Length 1072;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                       Query Match
4.8%; Score 179.5; DB 2;
Best Local Similarity 19.7%; Pred. No. 0.21;
Matches 164; Conservative 126; Mismatches 345;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

May 3, 2004, 19:27:02 ; Search time 8.2539 Seconds (without alignments) 4636.784 Million cell updates/sec

US-09-848-909A-13 3772 1 EVKQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 735 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NSD1 HUMAN	YNC7 YEAST	SRB9 YEAST	HLYA PROMI	HEX2 YEAST	CIC2_RAT	BXB CLOBO	RIFI YEAST	GLN3 YEAST	MYS3 SCHPO	YM41_YEAST	CNA_STAAU
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ALIGNMENTS

RESULT 1

PAGENTAL ID PAG BACAN STANDARD; PRT: 764 AA.	P13423; O9F5R7; O9KH69; O9ROU2;	01-UAN-1090	16-OCT-2001 (Rel. 40, Last	10-OCT-2003 (Rel. 42, Last annotation update)	Protective antigen precurso	(FAZU); FA-63	DACT ON FACTOR		Plasmid pxol.	OC BACCETIA; FIRMICUTES; BACILIALES; BACILIACEAE; BACILIUS.			SEQUENCE FROM N.A.	MEDLINE=89172073; PubMed=3148491;	Welkos	Schmidt J.J.;	"Sedne		Gene			RC STRAIN=28, 33, BA1024, and BA1035;	MEDLINE=99214082; PubMed=10197996;	Price L.B., Hugh-Jones M., Jackson P.J., Keim P.;	"Genetic diversity in the protective anti				RP SEQUENCE FROM N.A.	RC STRAIN=V770-NP1-R / ATCC 14185;	MEDLINE=20359347; PubMed=10899854;	Cohen S., Mendelson I., Altboum Z., Kobiler D., Elhanany	Leitner M., Inbar I., Rosenberg H., Gozes Y.,		"Attenuated nontoxinogenic and nonencapsu	RT anthracis spore vaccines protect against anthrax.";	Intect. Immun.	[4]	KF SEGUCINCE FROM N.A.		MEDDINESY9445483; PUDMed=LOSI5943;	OKINGA R.T., CIOUA K., Hampton O., Horrmaster A.K., Hill K.K.,	Neith F., Noenter 1.M., Danille G., Numaio S., Mairrion C., Mairrer	, Jackson P.J.;	"Sequence and organization or paol, the large Bacilius	KI plasmin narboring the Anthrax toxin genes.";		ے د		Singh V. Klimpel K.R. Ouinn C.P., Chaudhary V.K.,			receptor binding and anthrax toxin
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STRAIN=Sterne;
MEDLINE=95050722; PubMed=7961869;
Singh Y., Klimpel K.R., Arora N., Sharma M., Leppla S.H.;
Singh Y., Klimpel K.R., Arora S., Sinch S.H.;
The chymotrypsin-sensitive site, FFD315, in anthrax toxin protective antigen is required for transhocation of lethal factor.";
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MUTAGENESIS OF GLN-1512, ASP-541; LEU-543 AND ARG-621.
MUTAGENESIS OF GLN-1512, ASP-541; LEU-543 AND ARG-621.
MOSTIGE-21125576; PubMed-11222612;
MOSTIGGE J., MOUREZ M., Collier R.J.;
"Involvement of domain 3 in oligomerization by the protective antigen molecy of anthrax toxin.";

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MEDLINE-21092804; PubMed=11178978;
MEDLINE-21092804; PubMed=11178978;
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MUTAGENESIS OF PHE-581; PHE-583; ILE-591; LEU-595 AND ILE-603.
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MEDLINE=21438996; PubMed=11554763;
MEDLINE=21438996; PubMed=11554763;
MEDLINE=21438996; PubMed=11554763;
"Hydrophoble residues Phe552, Phe554, Ile562, Leu566, and Ile574 are required for oligomerization of anthrax protective antigen.";
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"Proteolytic activation of receptor-bound anthrax protective antigen on macrophages promotes Its internalization.";
Cell. Microbiol. 2:251-258(2000).
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STRAIN=Weybridge,
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BEDLINE=94131956,
No. Dai Z., Kaufman-Yarbray M.;
Regulation of the Bacilius anthracis protective antigen gene: CO2
a trans-acting element activate transcription from one of two
                                                                                                                          MEDLINE=94327640, PubMed=8051159,
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Abribrax protective antigen forms oligomers during intoxication of
mammalian cells.";
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[9]
MUTAGENESIS OF PHE-342; PHE-343 AND ASP-344.
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MUTAGENESIS OF TRP-375; MET-379 AND LEU-381.
   Biol. Chem. 266:15493-15497(1991)
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                                            EVKQENRILLNESESSSQGLIGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                         Gaps
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        Length 764;
      Score 3750; DB 1; Length 7
Pred. No. 1.4e-179;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IKKILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.5%;
Matches 731; Conservative
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NCBI_TaxID=1392;
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SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01.FBE-1996 (Rel. 33, Last sequence update)
01.OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P190).
MEDLINE-89172073; PubMed-3148491; Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Leppla S.H., Schmidt J.J.; Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis."; Gene 69:287-300(1988).
                                                                                                                                                                                                                                                                             Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K., Keim P., Koehler T.M., Lamke G., Kumano S., Mahilon J., Manter L Martinez Y., Ricke D., Svensson R., Jackson P.J.; Squence and organization of pxOl, the large Bacillus anthracis plasmid harboring the Anthrax tooxin genes."; Jacketing the Anthrax tooxin genes."; Jacketing I 81:6509-6515 (1999).
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KSCNCILIYVEVSQLMNSVFY -> NHVIVYLSM
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34.6%; Pred. No. 1.9e-05;
tive 36; Mismatches 47;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=86136024; PubMed=3004972; MEDLINE=86136024; PubMed=3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife Stunnenberg H., Bujard H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid; Transmembrane.
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MEDLINE=99445483; PubMed=10515943;
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                                                                                                                                                                     361 DSID-----TDINFA-----NDVLGYYKILSEKYKSDLDSIKKYINDKQGE 1401
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 381
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MEDLINE=86014355; PubMed=2995820;
Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V.,
Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
Freeman R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
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                                 1192 ESGSDTLEQSOPKKPASTHVGAES---NTITTSQ-NVDDEVDDVIIVPIFGESEEDYDDL
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NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTT----
                                                                       382 -SLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA----LNAQKDASSTPITMNYN
                                                                                             438 -----YNFENGRYRYDTGOV-YGNIAT-----YNFENGRYRYDTGSNWSEVL
                                                                                                                                                                                                                        482 PQIQETTARIIFNGKDLNLVERRIAAVNPSDPL-----ETTKPDM-TLKEALKIAFGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surface antigens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTM: Merozoite surface antigen contain the sequence of 83 KDa kDa and 19 kDa antigens which are the major surface antigens merozoites. The maturation take place during schizont.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum (isolate Wellcome).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5848;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite s
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                                                                                                                                                                         PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
                                                                                                   Pan W., Tolle R., Bujard H., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 "Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; Iransmembrane; GPI-anchor.
SIGNAL.
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REPEAT.
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Conservative 138; Mismatches 256;
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TRIPEPTIDE SG(TP) RI
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GermOnline; 142894; -.
SGD; S0004832; ESC1.
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STRAIN=S288C / AB972;
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                                            InterPro; IPR006209; EGF_like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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PIR; S05603; S05603.
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                                                                                                                               1525 INISQHQCVKK------QCPQNSGCFRHLDE-------REBCKCLLANYKQBGDKC- 1566
1466 IQDKLADFKKNNNFVGIADLSTDÝNHNNLLTKFLSTGMVFENLAKTVLSNLLDGNLQG-M 1524
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                                                                                   LNIDKD---IRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97313268; PubMed=9169872; Brown D., Chillingworth T., Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Liye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'YM67_YEAST STANDARD; PRT; 1658 AA.

603651, 204988.

10-007-1997 (Rel. 35, Created)

10-007-2003 (Rel. 42, Last sequence update)

110-007-2003 (Rel. 42, Last amnotation update)

Hypochetical 187.1 kDa protein in GUAI-ERG8 intergenic region.

YMR219W OR YM8261.13 OR YM9955.01.

Saccharomyces cerevisiae (Bakert's great).

Sucharomyces cerevisiae (Bakert)

Saccharomyces Saccharomyceties;
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8.6%; Pred. No. 0.66;
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GO; GO:0006348; P:chromatin silencing at telomere; IMP
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-----KVHEEETLFEANV 993
                                                                                                                                                            574 NLSGRSLDESEEQIPLKDF---TGENNNNLKTD-RGDLSSS---VEIEVEKV----SEKK 622
                                                                                                                                                                                                                                          LSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAD 397
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                                                            GYTVDVKNKRTFL---SPWISNIHE--KKGLTKYKSS-----PEKWSTASD-----
                                                                                       GYDVIGKSVESDLHEHSP--DNLYDLAARAMLQFQQSRNSNCPQKEEQVSESYLGHSNGS
                                                                                                                                       ------PYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQ
                                                                                                                                                                                                                STONTDSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Bukarycta; Fundi; Ascomycota; Saccharomycoties;
Saccharomycetales; Saccharomycetacee; Saccharomyces.
NGBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96220458; PubMed=8649382;
Luke M.M., della Seta F., di Como C.J., Sugimoto H., Kobayashi
Arndt K.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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Cell. Biol. 16:2744-2755(1996)
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STRAIN=5288c / AB972;
MEDLINE=95400292; PubMed=7670463;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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TYSKSNYMIRDCFQNN -> DLFKIKLYDTRIVSKIM (IN
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                                                                                                                                                                                                                                                                                                            Exi T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I.,
Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.,
Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.,
"Analysis of a 36.2 kb DNA sequence including the right telomere of
chromosome VI from Saccharomyces cerevisiae.",
Yeast 12:149-167(1996).
-!- FUNCTION: Associates with the SIT4 phosphatase in a cell cycle
dependent manner. May be directly or indirectly involved in
SIT4-dependent functions in budding and in normal G1 cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262;
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SSN -> PDIQVI (IN REF. 2 AND 3)
AD4FBF0BC7C588D5 CRC64;
   Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Teuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T., "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

4.5%; Score 168; DB 1; Length 1000;
Best Local Similarity 19.5%; Pred. No. 0.37;
Matches 173; Conservative 128; Mismatches 323; Indels 26
Ozawa
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DY -> EL (IN
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MEDLINE=96287652; PubMed=8686379;
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                                                                                                                                Saccharomyces cerevisiae.";
Nat. Genet. 10:261-268(1995)
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InterPro; IPR007587; SAPS.
Pfam; PF04499; SAPS; 1.
Phosphorylation; Cell cycle.
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498
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                                                                                                                                                                                                                                                                                                   TVGT-----YSKSNYMIRD---CFQNNELFLTHPWNNFWHNVIFDIIQQIFNGR
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                                                              GLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNY
                                                                                                         411 YPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKOLRLDTDQVYGNIATYNFENGRVR
                                                                                                                        471 VDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNP--SDPLETTKPDMTL--KBA
                                                                                                                                                                                             -----VELIAELLHCSNWGLMNSKRAERIARRRDKVRSQLSHHLQDALNDLSIEEKEQ
                                                                                                                                                                                                                        LKIAFG------PNEPNGNLQYQCKDI-----TEFDFNFD---QQTSQNIKNQLAE
                                                                                                                                                                                                                                                   LKTKHSPTRDTDHDLKNNNGKIDNDNNDNDDBSDYGDEIDESFEIPYINMKQNIKLRTDP
                                                                                                                                                                                                                                                                                                                                          ---SSTEGLLLNID--KDIRKILSGYIVEIE---DTEGLKEVINDRYDMLNISS---LR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sunagawa H., Ohyama T., Watanabe T., Inoue K.; "The complete amino acid sequence of the Clostridium botulinum type neurotoxin, deduced by nucleotide sequence analysis of the encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium botulinum.
Bacteria, Firmicutes; Clostridia, Clostridiales, Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurotroxin type D precursor (EC 3.4.24.69) (BONT/D)
(Bontoxilysin D).
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STRAIN=D-24, and D-1873;
MEDLINE=8939741; PubMed=2668193;
Moriishi K., Syuto B., Kubo S., Oguma K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1276
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MEDLINE=91016853; PubMed=2216736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vet. Med. Sci. 54:905-913(1992)
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MEDLINE=93042276; PubMed=1420572;
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  Length 1276;
Query Match
4.4%; Score 166; DB 1; Length 127
Best Local Similarity 20.7%; Pred. No. 0.65;
Matches 165; Conservative 117; Mismatches 290; Indels
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Saccharomyces cerevisiae (Baker's yeast). Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales; Saccharomycetaceae, Saccharomyces.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 NEDOSTQNTDSETRIISKN--TSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 VAIDHS-----LSLAGERT-WAETMGLNTADT-ARLNANIRYVNTGTAPIYNVLP-TTSL
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STRAIN=S288C / FY1679;

BDDLINE=97103775; bubMed=8948101;

Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;

Cziepluch C., Kordes E. a 40.2 kb fragment of yeast chromosome X
"Sequencing analysis of a 40.2 kb fragment of yeast chromosome X
reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2,
SPT10, GCD14, RPE1, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes,
three remnant delta elements and a Ty4 transposon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LDTDQVYGNIATYNFENGRV----
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ilarity 19.5%; Pred. No. 1.2;
Conservative 123; Mismatches 274; Indels 270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16DCD7284A8D52D3 CRC64;
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SGD; S0003649; YUL113W.
InterPro; IPR001584; Rve.
InterPro; IPR001581; Znf_CCHC.
Pfam; PF00665; rve; 1.
SWART; SW00343; Znf C2HC; 1.
Transposable element; Hypochetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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es 162; Conserv
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KEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKL 583
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MEDLIFE=20107136; Pubmed=10639340;
IKemoto S., Nakamura T., Kibinoda C.;
"S. pombe sporularion-specific coiled-coil protein Spo15p is localized
"S. pombe sporularion-specific coiled-coil protein Spo15p is localized
to the spindle pole body and essential for its modification.";
J. Cell Sci. 113:545-554(2000).
                                                 --GELNYV-RHKCRYDIEFAVKKVARLVNYPHERVFYMIYKIIQYL--
                                                                                                                                                  ----VRYKDIGIHYDRDCNKDKKVIAITDASVGSEYDAQSRIGVILWYGMNIFNVYSNK
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MEDLINE=20223868; PubMed=10759889;
Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                              ---DFKKY 681
                                                                                                584 NAKMNILIRDKRFHYDRN-----NIAVGADESVVKEAHRE----VI-
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010411; Q9USE9;

01-077-1996 (Rel. 34, Last sequence update)

01-0C7-1996 (Rel. 34, Last sequence update)

10-0C7-1996 (Rel. 42, Last annotation update)

10-0C7-2003 (Rel. 42, Last annotation update)

Sporulation-specific protein 15.

SPOIS OR SPACHES.06C.

SChizosaccharomyces pombe (Fission yeast).

Schizosaccharomycetales; Schizosaccharomycetes;

Schizosaccharomyces.

NCBI_TAXID=4896;
                                                                                                                                                                                                                                                                                                                -----EVINDRYDMLNISSLRODGKTFI
                                                                                                                                                                                                         STEGLLLNIDKDIRKILSGY-------
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ENIILSKNEDQSTQNTD---SETRTISKNTSTS----RTHTSEVHGNAEVHASFFD 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  316 IGGSVSAGFSNSNS----STVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            417 SYDKMYKOVSSQLEEARSSLAHATGKLAEINSERDFQNKKIKDFEKIEGDLRACLNSSSN 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQE 486
            "Large-scale screening of intracellular protein localization in living fisation yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).
-1. FUNCTION: Has a role in the initiation of spore membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 LTNMESNFSAKÓSBAYDLSRQLLTVTEKLDKKEKDYEKIKEDVSSIKASLAEBGASNKSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 LENIPSENQYFQSAIWS---GFIKV----KKSDEYTFATSADNHVTMWVDDQEVINKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 NSNKIRLEK---GRLYQIKIQYQRENPTE---KGLDFKLYWTDSQNKKEVISSDNLQLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 RGEQERLEKLLVSSNKTVSTLROTENSLRAECKTLOEKL-----EKCAINEEDSKLLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156 LKOKSSN-----SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---FOEKLAKSVMOLKENEONFSSLDTSFKKLNESHOELENNHOTITKOL--
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MM; 3F480CA06171D9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 132; Mismatches 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , DB 1;
1.5;
                                                                                                -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LOCATION: Spindle pole body.
-1- SIMILARITY: Belongs to the MPC70 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.3%; Score 164;
0.4%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                        EMBL; AB027811; BAA87115'1;
PIR; T38077, T38077
GeneDB SPombe; SPACIF3.06c;
Sporulation; Colled coil.
COMAIN
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1723
A; 222785 N
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1481 172
1957 AA;
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SA MEDINEE-21848801; PubMed=11859360;

RA Goullins M., Hayles J., Lyne M., Lyne R., Stewart A.,

RA Goullins W., Canel N., Hayles J., Chillingworth T., Churcher C.M.,

RA Goullins M., Connor R., Cronin A., Davis P., Feltwell T., Farser A.,

RA Gentles S., Gobne A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA James K., Ones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., Ones L., Jones M., Leather S., McDonald S., McLean J.,

RA James K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,

RA Joney P., Moule S., Saunders B., Squares S., Stevens K.,

RA Liver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch B.,

RA Skelton J., Simmonds M., Squares B., Stevens K.,

RA Skelton J., Stanger R., Squares S., Stevens K.,

RA Skelton J., Stanger B., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,

RA Gotfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Gotfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Ber P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Gotfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,

RY "The genome sequence of Schizosaccharomyces pombe.";

RY "The genome equence of Schizosaccharomyces pombe.";
TTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDM-TLKEALKI----AFGFNEPNGNLQ 541
                                                                                                                                                                                                               -----AMKQSFTSLVNSYQS--ISNLYHELRDDHVNMQSQNNTLLESESKLKTDC 824
                                                                                                                                                                                                                                                         EGLKE----VINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENT 706
                                                                                                            SNKSLIKKQEDVDSLEKNI-------QTLKEDLRKSEEALRFSKLEARNLREVIDNL-
                                                                                   YOGKDIT-EFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
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Mol. Biol. Cell 11:647-661(2000).
-!- FUNCTION: Involved in the organization and/or function of
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Jin H., Amberg D.C.;
"The secretory pathway mediates localization of the cell
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013735, Q9UTJ0,
013735, Q9UTJ0,
16-UL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBS-2003 (Rel. 41, Last annotation update)
Actin interacting protein 3 homolog.
FATI OR SPACISAIO.16 OR SPACISEI.01.
Schizosaccharomyces pombe (Fission yeast).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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1385 AA; 154325 MW; ABB3D40CC4FF7537 CRC64;
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A Galibert F., Alexandraki D., Baur A., Boles E., Chalwatzis N.,

Galibert F., Cocerer F., Catepluch C., De Haan M., Domdey H.,

A Chuat J.-C., Coster F., Gatius M., Goffeau A., Grivell L.A.,

A Hennemann A., Herbert C.J., Heumann K., Hilger F., Hollenberg C.P.,

A Huang M.-E., Jacq C., Jauniaux J.-C., Katsoulou C., Kirchrath L.,

Kleine K., Kordes E., Koetter P., Liebl S., Louis E.J., Manus V.,

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Zollner A., Karpfinger-Hartl L.,

"Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOTA1-788(2002).

TUNCTION: Involved in chromosome cohesion during cell cycle and in DNA repair. Central component of cohesin complex. The cohesin complex is required for the cohesion of sister chromatids after DNA replication. The cohesin complex apparently forms a large proteinsceous ring within which sister chromatids can be trapped. At anaphase, the complex is cleaved and dissociates from chromatid, allowing sister chromatids to segregate.
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MEDLINE-99145468; PubMed-990856;
Toth A., Closk R., Uhlmann F., Galova M., Schleiffer A., Nasmyth K.;
"Yeast cohesin complex requires a conserved protein, Ecolp(Ctf7), to establish cohesion between sister chromatids during DNA replication."; Genes Dev. 13:320-3331(199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97474309; PubMed=9335333;
Michaelis C., Ciosk R., Nasmyth K.;
"Cohesins: chromosomal proteins that prevent premature separation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [5]
IDENTIFICATION IN A COHESIN COMPLEX WITH SMC3; MCD1 AND IRR1, AND
                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Structural maintenance of chromosome 3 (DA-box protein SMC3).
SMC3 OR VIL074C OR J1049.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycetines; Saccharomycetales; Saccharomycetales; Saccharomycetales; Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of the Compared of
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                                               EGLKEVINDRYDMLNISSLRQDGKTFI------DFKK----YNDK
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STRAIN=S288c / FY1678;
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Cell 91:35-45(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- SUBUNIT: Cohesin complexes are composed of the SMC1 and SMC3 heterodimer attached via their hinge domain, MCD1/SCC1 which link them, and IRR1/SCC3, which interacts with MCD1. The cohesin complex also interacts with SCC2, which is required for its association with chromosomes.
-!- SUBCELLULAR LOCATION. Nuclear protein. Associates with chromatin. Before prophase it is scattered along chromosome arms. At anaphase, the MCD1 subunit of the cohesin complex is cleaved, leading to the dissociation of the complex from chromosomes, allowing chromosome separation.
-!- DOMAIN: The flexible hinge domain, which separates the large intramolecular coiled coil regions, allows the heterotypic interaction with the corresponding domain of SMC1, forming a viame of the corresponding domain of SMC1, forming a connected by different ends of the cleavable MCD1 protein, forming a ring structure (89 similarity).
-!- SIMILARITY: Belongs to the SMC family. SMC3 subfamily.
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REMBL; X24349; CAA61313.1; ---
REMBL; Z43449; CAA61313.1; ---
REMBL; Z56850; S56850; CAA61313.1; ---
REMBL; Z56860; S56850; S56850; CAA61313.1; ---
REMBL; Z68861; S68861; CAA61313.1; ---
REMBL; Z68861; S68861; CAA61313.1; ---
REMBL; Z68861; SAGC, SAGC, CAA61313; ABC, CAA61313; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; ABC, CAA61319; CAA61319; CAA61319; Colled coil; CAA61319; CAA61319; CAA6131; CAA61319; CAA61319; CAA6131; CAA61319; CAA61319; CAA6131; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA61319; CAA6131319; CAA61319; CAA61319; CAA61319; CAA61319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA6131319; CAA
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19.7%; Pred. No. 1;
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172 482 COILED COLL (POTENTIAL).
483 684 FLEXXBLE HINGE.
685 1041 COILED COLL (POTENTIAL).
1126 1161 ALA/ASP-RICH (DA-BOX).
1230 AA; 141336 MW; B152D89F7780341F CRC64;
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                                                                                                                                       GRUTF--IPLNRLSLDSDVKFPSNTTTQIQFTPLIKKIKYEPRFEKA-----VKHVFGKT
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 DHSLSLAGE-----LNTADTARLNANIRYVNTG
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01-FEB-1996 (Rel. 33, Last seq.
28-FEB-2003 (Rel. 41, Last anno
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIKYKSSPEKWSTASDPYSDFEKVIGRID--KNVSP-----EARHPLVAAYPIVHV
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Local Similarity 19.0%; Pred. No. 0.86;
Les 176; Conservative 132; Mismatches 342; Indels 275; Gaps
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                                                                                                                                                                                                                                                                                                                    39 ATP (POTENTIAL).
224 COLLED COLL (POTENTIAL).
400 COLLED COLL (POTENTIAL).
821 COLLED COLL (POTENTIAL).
912 ALA/ASP-RICH (DA-BOX).
110566 MW; 30D51C56B56280F4 CRC64;
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                                                                   EMBL; M34956; AAA25423.1; -.
PIR; JQ0894; JQ0894.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003439; GTP-bindding_dom.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_C.
Fam; PP02463; SMC_C; 1.
Fam; PP02463; SMC_C; 1.
TIGRFAMS; TIGR00650; MG442; 2.
ATP-binding; Coiled coil.
NP BIND 32
DOWAIN 169 224 COILED COILED
  entities requires a license agreement (or send an email to license@isb-sib.ch)
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WAPA BACSU
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                                                                              689
                                                                                             KEVINDRYDMLNIS---SLRQDGKTFIDFKKYND-------KLPLYI--
                                   598 YDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKD-----IRKILSGYIVEIEDTEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li M.B., Neigeborn L.;
Unpublished observations (XXX-1997).
-!- FUNCTION: NOT KNOWN; NEGATIVE REGULATOR OF BARLY MEIOTIC GENE
                                                                                                                                                                                                                                                                                             Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1487;
                                                                                                                                                                                                                                                                                                                                                                                              "Sequencing of a 40.5 kb fragment located on the left arm of chromosome VII from Saccharomyces cerevisiae.";
Yeast 13:55-64(1997).
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TRAIN=S288c / FY1679;
MEDLINE=7197971; PubMed=9046087;
Coglievina M., Klima R., Bertani I., Delneri D., Zaccaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             768AEFBAB796E447 CRC64;
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                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
MDS3 protein (MCK1 dosage suppressor 3).
MDS3 OR YGL197W OR G1307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 160.5; I
Pred. No. 1.5;
                                                                                                                                                                                                         1487 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPRESSION.
-!- SIMILARITY: Contains 3 Kelch repeats.
-!- SIMILARITY: TO YEAST YER132C.
                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
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KELCH 2.
KELCH 3.
                                                                                                                            706
                                                                                                                                                  931
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                                                                                                                            ------SNPNYKVNVYAVTKENT
                                                                                                                                                  EVEAALDESNVIRYVEFLKLLKENT
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Kelch repeat; Repeat; Meiosis.
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                                                                                                                                                                                                          STANDARD;
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Germonline; 141245; -.
TRANSFAC; T03484; -.
SGD; S0003165; MDS3.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1064 YSILAKKEESLSLICTSLMETFRİKTLNSYKGDEBKTNTYLTSNDNYQELLK--LKVSLE 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDQQTSQNIKN-QLAELN-----ATNIYT------VLDKIKLNAKMILIRD 593
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                                                                                                                                                                                                                                                                                                                                                                                               EARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEV 309
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                                                                                                                                                                                                                                                                                                                                                 310 HASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNT
                                                                                                                                                                             107 RLEKGRLYQ--IKIQYQRENPTEKGLDFKLYMTDS---QNKKEVISSDNLQLPELKQKSS
                                                                                                                                                                                                      902 KASPFSSRRSSHIG---RRSSTPETENAFS-ATPRA-----SLDGOMLGKSLKEGST
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                                                                   610 VROEGRL-----SSSGSLDNYF-EKNF--PIFARTSVSEAQNTOPQVANADAKAPNTPS
                                                                                                    56 BNQYFQSAIWSGFIKVKKSDEYTFATSADNHVTWWV-----DDQEVIN--KASNSNKI
                                                                                                                               202 FLSP------WISNIHEKKGLTKYKSSPEKWSTASDPYSDPEKVTGRIDKNVSP
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   Indels
   175; Conservative 134; Mismatches 286;
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01-0CT-1994 (Rel. 30, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Wall-associated protein precursor.
WAPA OR NIG OR BSU39230.
Bacillus subtilis.
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MEDLINE-98044033; PubMed=9344377;

Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Moszer I., Bolotin A., Borchert S.,

Borriss R., Bourstier L., Brans A., Braun M., Brighell S.C., Bron S.,

Browillet S., Bruschi C.V. Caldwell B., Capuano V., Carter N.M.,

R. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Daniel R.A.,

Brois S.K., Codani J.J., Connertoff A., Ehrlich S.D., Emmerson P.T.,

R. Benizot F., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

R. Entian K.D., Errington J., Fabret C., Frerariz E., Foulger D.,

R. Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

R. Aniseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Haiech J., Lazarevo C.R.,

R. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Kobayashi Y., Koetter P., Komingstein G., Krogh S., Kumano M.,

R. Kobayashi Y., Koetter P., Mizuno M., Mosell D., Nakai S., Noback M.,

R. Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Presoct R.A.,

R. Noore D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

R. Presecan E., Pujic P., Purnelle B., Ropbort G., Rey M., Reynolds S.,

R. Schiguchi J., Sekowska A., Sercor S.J., Serror P., Shin B.S.,

Schiguchi M., Tamakoshi A., Tanaka T., Takahashi H., Takemaru K.,

R. Atsuchi M., Tamakoshi A., Tanaka T., Tarahashi H., Takemaru K.,

R. Atsuchi M., Tamakoshi A., Tanaka T., Teror P., Shin B.S.,

A Viari A., Wambutt R., Wadler B., Wedler H., Weitzenegger T.,

R. Winters P., Wiphiwam S., Vandenbol M., Vannier F., Vassarotti A.,

Viari A., Wambutt A., Yanamoto H., Yamanethi E., Yoshikawa H., Danchin A.,

R. Walbelle, S., Wandenbol M., Wannier S., Vassarotti A.,

R. Willers P., Walbelle, S., Sunketin B., Roshilas H., Pakenerium Bacillus

R. Walbelle, S., Socielle B., Roshilas B., Roshilas B., Park S.,

R. Walbelle, W., Wannanco Of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 390:249-256(1997).
--:- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,
MOTILITY, SECRETION OR DIFFERENTIATION.
--:- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED
INTO THE MEDIUM.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=168 / BGSCOLA1;

MEDLINE=95219088; PubMed=7704263;

Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;

Tcloning and sequenching of a 29 kb region of the Bacillus subtilis

genome containing the hut and wapA loci.";

Microbiology 141:337-343(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURNCE FROM N.A.

STRAIN=168 / BGSC1A1;

MEDLINE=97124196; PubMed=8969509;

Voshids X.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,

Niwa Y., Fujita Y.;

"Sequencing of a 65 kb region of the Bacillus subtilis genome

containing the lic and cel loci, and creation of a 177 kb contig

covering the gnt-sacxy region.";

Microbiology 142:3113-3123(1996).
                                                                                                                                                                "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of
gene encoding a 258 kDa precursor two-domain ligand-binding
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98044033; PubMed=9384377;
                                                                                                    STRAIN=168;
MEDLINE=93302506; PubMed=8316082;
                                                                                                                                                                                                                                                                  Mol. Microbiol. 8:299-310(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=168;
                                                                     SEQUENCE FROM N.A.
               NCBI_TaxID=1423;
                                                                                                                                                                                                                                                protein.";
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DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.

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42;
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                                                                                                                                                                                                         R BMEL; 105634; AAA22883.1; -
R BMEL; 105634; BAA66656.1; -
R BMEL; D32985; BAA66650.1; -
R BMEL; D32926; BAA1683.1; -
R BMEL; 259124; CAB15959.1; -
R PIR; 323220; 332320; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS3230; AS
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
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4.3%; Score 160.5; DB 1; Length 3
Best Local Similarity 18.2%; Pred. No. 2.8;
Matches 173; Conservative 125; Mismatches 337; Indels
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2334 AA; 258329 MW;
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                                                             329 ITINYSASSOKWDANLKAYVLKTGYYD-KTTGTNYAFMKFINNLKPIONMTVTKATLKTYVA 387
                                                                                                                                          ------WVDDQEVINK------ASNSNKIRLEKGR--LYQIKIQYQR 122
                                                                                                                                                                                                            388 HSYYGTKATGLWLD---TVNSNYDNAKVTWNTKPASKNIGKADVHKGQWASYDVTAAVKS 444
                                                                                                                                                                                                                                                                                                                                                                                                                             177 -----DRDNDGIPD----SLE-VEGYTVDVKNYRTFLSPWISNIHEKKGLTKYKSSP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 KKIWPTSAEIASKRYKI.--HLDGKDGAELALDP----SPVYKNSGGSYATSKNYMIGVSA 599
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SENQYFOSAIWSGFIK -- VKKSDEYTFATSADNHVTM --
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytotoxicity associated immunodominant antigen (120 kDa protein)
CAGA OR CAI OR CAG26 OR JHP0495.
Helicobacter pylori J99 (Campylobacter pylori J99),
Bacteria, Proteobacteria; Epsilonproteobacteria; Campylobacterales;
STANDARD;
CAGA HELPJ
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  535 GFSKVAVFNLPNLINILAITSV----VRQDLEDKLIAKGLSPQEANKLVKDFLSSNKELVG 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KASNSNYIRLE --- KGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPE 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 HEKKGLTKYKSSPEKWSTASDPYSDFEK-----VTGRI-DKNVSPEARHPLVAAYPIV 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        742 --KVENLNAALNEFKNGKNKDFSKVTQAK--SDLENSIKDVIINQKITDKVDNLNQAVSV 797
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                                                                                                                                                                                                                                                                                      -!- FUNCTION: MAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING, EXPORT, OR FUNCTION OF THE CYTOTOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636 LESKSGNKNKMEAKSQANSQKDEIFALINKBANRDARAI-AYAONLKGIKRELSDKLENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               798 AKATGDFŚGV------EQALADLKNFSKEQLAQQAQKNEDFNTGKNSALYQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   591 KALNFNKAVABAKNTGNYDEVK---QAQKDLEKSL------KKRERLEKDVAK--N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 LKOKSSNSRKKRSTSAGPTVPDR----DNDGIPDSLEVEGYTVDVKNKRTFLSPWISNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 GFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTG-TAPIYNVLPTT
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                                                                               MEDLINE=99120557; PubMed=9921682; Alm R.A., Ling L.S., Doig P.C., Alm R.A., Ling L.S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Guilde, deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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                                                                                                                                                                                                                  "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167; Conservative 138; Mismatches 297; Indels 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.2%; Score 158.5; DB 1; Length 1167; 20.5%; Pred. No. 1.4;
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129729 MW; FD5E86B81CEBD0F2 CRC64;
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InterPro; IPR004355; IVSec_cagA.
Helicobacteraceae; Helicobacter.
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PRINTS; PR01553; TYPE4SSCAGA.
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                                                            SEQUENCE FROM N.A.
                     NCBI_TaxID=85963;
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Search completed: May 3, 2004, 19:37:04 Job time : 13:2539 secs

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Q897h6 clostridium Q26216 plasmodium Q26216 plasmodium C015579 helicobacte Q1109 plasmodium Q81472 plasmodium Q81548 plasmodium Q81548 plasmodium Q81548 plasmodium Q81549 plasmodium Q8154 plasmodium Q917445 plasmodium Q774ve6 plasmodium Q9174 ataphylococ Q9116 ataphylococ Q9116 ataphylococ Q9116 ataphylococ Q11621 plasmodium Q81549 plasmodium Q81549 plasmodium Q81549 plasmodium Q81649 plasmodium Q81649 plasmodium Q81100 plasmodium Q81100 plasmodium Q81100 plasmodium Q81100 plasmodium Q81100 plasmodium Q81100 plasmodium Q81491 plasmodium Q81491 plasmodium Q814100 plasmodium Q814100 plasmodium Q8141100 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q814171 plasmodium Q8
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97.6%; Score 3681; DB 2; Length 741;
Best Local Similarity 99.3%; Pred. No. 5.3e-167;
Matches 717; Conservative 1; Mismatches 4; Indels (
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                           QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                      QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                               QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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0937W3 01-DEC-2001 (TrEMBLEI. 19, C
01-DEC-2001 (TrEMBLEI. 19, L
01-JUN-2003 (TrEMBLEI. 24, L
Pag protein (Fragment).
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Bacteria; Firmicutes;
NCBI TaxID=1392;
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Pred. No. 5.3e-167;
1; Mismatches 4;
EMBL, AJ413936, CAC93934.1; -. GO, GO:0005576; C:extracellular; IEA. GO, GO:0046821, C:extrachromosomal DNA; IEA. GO, GO:0015070; F:toxin activity; IEA. GO, GO:0009405; P:pathogenesis; IEA. InterPro; IPR03896; Anthrax toxinB. Pfam; PF03495; Binary toxB; I. PRINTS; PR01391; BINARATOXINB.
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63 AIWSGFIKVKKSDEYTFATSADNHVTWMVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR 122
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                    NIYTVLDKIKLNAKMNILIRDKRFHY---DRNNIAVGADESVVKEAHREVINSSTEGL--
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Gibert M., Perelle S., Daube G., Popoff M.R.;

"Clostridium spirofcrme toxin genes are related to C. peri "Clostridium spirofcrme toxin genes are related to C. peri Syst. Appl. Mcrobiol. 20:337-347(1997).

R MRL; X97969; CAA66612.1; -. HSP; P13423; 1ACC.

R GO; GO:000556; C:extracellular; IEA.

R GO; GO:000556; C:extracellular; IEA.

R GO; GO:0009459; P:toxin activity; IEA.

R DFAn; PRO3495; Binary toxin B.

R PFAn; PRO3495; Binary toxin B.

R PRINTS; PRO3191; BINARYCOXINB.

SEQUENCE 879 AA; 98739 MW; 40685ACB8E05BA01 CRC64;
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01-JAN-1998 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Bacteria, Firmicutes, NCBI TaxID=29348;
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                                                                                                                                                           Clostridium difficile.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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                    01-JAN-1998 (TrEMBLrel, 05, 01-JAN-1998 (TrEMBLrel, 05, 01-JUN-2003 (TrEMBLrel, 24, ADP-ribosyltransferase,
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                                        LSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAD
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A Chang S.Y., Song K.P.;
"ADP-ribbesylating Binary Toxin Genes of Clostridium difficile stratic CCUG 20309.";
"CCUG 20309.";
Submitted (MAY-2000) to the EWBL/GenBank/DDBJ databases.

R SSP; P13423; 1ACC.
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:toxin activity; IEA.
GO; GO:0009405; P:toxin activity; IEA.
R GO; GO:0009405; P:phrex toxinB.
R PRINTS; PR01391; BINARY_COXIB.
R PEMINTS; PR01391; BINARY_COXIB.
CEQUENCE 876 AA; 98793 MW; 3660627352E745A5 CRC64;
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Last annotation update)
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01-OCT-2000 (TrEMBLrel. 1:
01-UTN-2003 (TrEMBLrel. 2:
CdtB.
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01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
10-ta toxin component Lb precursor.
Clostridium perfringens.
Bacteria; Firmicutes, Clostridia, Clostridiales, Clostridiaceae;
Clostridium.
NCBI_TaxID=1502;
                                                                       125;
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Query Match 23.1%; Score 872.5; DB 2; Best Local Similarity 31.4%; Pred. No. 1.7e-33; Matches 250; Conservative 139; Mismatches 281;
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                                                                                                                                                                                                       Popoff M.R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
BMBL; X73562; CAA51960.1; -.
PIR; 140862; IAGG.
HSSP; P13423; IAGC.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015076; F:toxin activity; IEA.
GO; GO:0015076; F:toxin activity; IEA.
InterPro; IPRO3986; Anthrax toxinB.
Pfam; PF03495; Blnary LoxB; I.
PRINTS; PR01391; Blnary LoxB.
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C9AE092CD3818921 CRC64;
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212 875 IC
875 AA; 98468 MW;
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175 SNAKLKANANRDTDRDGIPDEWEINGYTVWNQKAVAWDDKFAAN----GYKKYVSNPFK 230 700 EKDYTKESYEFETTGKDSSDIEITLTSGGVIFLÖNLSITELNSTPEILKEPEIKVPSDQE 759 62 The Size And Component of the Component of the Component of the Component of the Component of the Component of the Component of Compone DGLQSVANKLSGETKIIIPMSKLKPYKRYVPSGYSKDPSTSNSITVNÍKSKÈQKTDYLVP ---KLERGMNILIKVPSYFTNFDEYNNFP--ASWSNIDTKNQ -- IVEIEDTEGLKEVIND 3 KQENRLLNESES--SSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 61 OSAIWSGFIKVKKSDEYTFATSADN-HVTMWVDDQEVINKASN-SNKIRLEKGRLYQIKI 119 -QYQRENPTEKGLD-FKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTV-------PDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEK --SLRQDGKTFIDFKKYND--KLPLYISNPNYKV----꿈. 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
02 toxin (Component-II).
Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridian.
Clostridium.
NCBI_TAXID=1491; E., Fujii N.; Length 721; Query Match
21.5%; Score 810; DB 2; Length 72
Best Local Similarity 35.3%; Pred. No. 1.2e-30;
Matches 223; Conservative 117; Mismatches 228; Indels SEQUENCE FROM N.A.
STRAIN=LYPE C;
MEDLINE=98323874; PubMed=9659689;
Kimura K., Kubota T., Ohishi I., Isogai H., Isogai E
Mimre gene for component II of botulinum C2 toxin.";
Vet. Microbiol. 62:27-34(1998). EVINSSTEGL ------LINIDKDIRKILSGY --760 ILDAHNKYYADIKLDT----NTGNTYIDGI 785 Ä 721 -----NVYAVTKENTIINPSENGDTSTNGI PRT; IIKEQLKYLDDKKIYNV--PRELIMINARY; 659 RYDMLNIS---

g õ Db $\dot{\diamond}$ g δ СD $\stackrel{\diamond}{\circ}$

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396 ADENQLSQILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------NSAEAHSNNSYTYANSE------GASIEAGFGPKGFSFGVSANYOHTET 366
                                                                                                                                                                                                    340 LAGERTW----AETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    562 IKNQLAELNATNIYTVLDKIKLNAKANILIRDKRFHYDRNNIAVGADESVVKEAHREVIN 621
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                                                                                                                                                                                                                            216 QKMKRDIDED---TDTDGDSIPDLWEENGYT--IQNK--VAVKW-DDKFAQQGYVKYLSS
                                         PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
                                                                                                                      283 DSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS
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STRAIN-A2012;
MEDLINE-22064136; PubMed=120044073;
MEDLINE-22064136; PubMed=120044073;
MEDLINE-22064136; PubMed=120044073;
Mead T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
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Science 296:208-2031(2002).
GO:0046821; C:extrachromosomal DNA, IEA.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
Protective antigen-related protein, (pX01-111).
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Bacillus anthracis.
Plasmid pXO1.
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Les 68; Conserv
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NCBI_TaxID=1392;
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Q8KYK2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SD--TKFNIDSKTFKEFKLFKIDSQNQSQQVKRDELRNPEFNKKESREFLAKASKTNFFM 215
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                                                                                                             344 --IGE-SPSQGLSINTGESAYINPNIRYYNTGTAPVYNVTPTTIVIDK-QSVATIKGQE 399
                                                                                                                                                                                                                                                  399 NQLSQILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGN 458
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                                                                                                                                                                                                                                                                                                                                                                                                                  TKPDMTLKEALKIAFGFNEPNGNLQYQGKDIT---BFDFNFDQQTSQNIKNQLAELNATN 573
                                                                                                                                                                                                                                                                                                                                                                                                                                            TRIISKNISTSRIHISEVHGNAEVHASFFDIGG-----SVSAGFSNSNSSIVAIDHSL 338
                                                                                                                                                                    SLAGERTWAETWGLNTADTARLWANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADE 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shi Y., Chen J., Pang Y.;
"Cloning of viplA(C) and vip2A(C) from Bacillus thuringiensis HD201.";
"Cloning of viplA(C) and vip2A(C) from Bacillus thuringiensis HD201.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AY245547, AA086514.1;
GO; GO:005576; C:extracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IFR03896; Anthrax_toxinB.
Pfam; PF03495; Binaty toxB; I.
PRINTS; PR01391; BINATYTOXINB.
SEQUENCE 775 AA; 87110 MW; 416B25394361B731 CRC64;
                              459 IATYNFENGRVRVDIGSNWSEVLPQIQETTARII--FNGKDLNLVERRIAAVNPSDPLET
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VIPLAC.
Bacillus thuringiensis.
Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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Matches 223; Conserv
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SEQUENCE FROM N.A.
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MEDLINE=22255705, PubMed=1236864,

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A Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W.,

A Carlton J.M., Paln A., Nelson K.E., Bowman S., Paulsen I.T., James K.,

Esten J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,

Chan M.-S., Nene V., Shallom S.J., Sub E., Peterson J., Angiuoli S.,

Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,

Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,

Morfadden G.L., Cummings L.M., Subramanian G.M., Mungall C.,

Perser C.M., Barrell B.;

"Genome sequence of the human malaria parasite Plasmodium

"I falciparum.";

Nature 419:498-511(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    671 DGKTF-----IDFKK--YNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNGIK 722
                                                                                                                                                   294 STSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVA---IDHSLSLAGERTWAETM 350
                                                                                                                                                                                                                            351 GLNTAD-----TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADENQLSQ 403
                                                                                                                                                                                                                                                                                                     ILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYN 463
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                                                                                                 544 SNNLSSNNINNSKNIFVNGNLKISNNLNNSGVIEGLELNTNSIENTGNITIKNKLISQNL
                      604 NNKK-----NTANYNAGFLDVHNKISS-VGNIKAITMKTNNLDNSGNIL-----TN
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---IPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKV
                                                                          TGRIDKNVSPEARHPLVAAYPIVHVDMEN-----IILSKNEDQSTQNTDSETRTISKNT
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OBILO4;
OBILO4:
O1-MAR-2003 (TrEMBLrel. 23, Created)
O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Hypothetical protein.
PRII_0371.
Elasmodium. falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NUSI_TAXID=36329;
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    MESLGINNIYNALDRIKLNAKMNILVRDP-YHYDNNGNIVGVDDSYLKNAYKQILNWSSD 59
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STRAIN=ATCC 25586;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,

Larsen N., D'Souza M., Waluns T., Pusch G., Haselkorn R.,

Ronstein M., Kyrpides N., Overbeek R.;

Genstein M., Kyrpides N., Overbeek R.;

Tolenome sequence and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium Fusobacterium and analysis of the oral bacterium fusobacterium and analysis of the oral bacterium fusobacterium and analysis of the oral bacterium fusobacterium and analysis of the oral bacterium fusobacterium and analysis and peptidolysis, IEA.

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InterPro: IPRO006508; Haemagg_act.

InterPro: IPRO006508; Haemagg_act.

InterPro: IPRO006508; Paptidase_226.
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                                          GLLLNIDKDIRKILSGYIVEIEDTE------GLKEVINDRYDMLNISSLRQDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
NCBI_TaxID=76856;
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Pfam; PF00018; SH3; 1.
PROSITE; PS00761; SPASE_I_3; 1.
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                                                                                                                                                                                                                                                                                                               ---DMENIILSKNEDQSTQNTD--SETRTISKNTSTSRTHTSEVHGNAEVHA--SFFDIG
                                                                                                                                                                                                                                                                                                                                           367 -VNTGTAPIYNVLPTTSLVLGKNQ------TLATIKADE--NQLSQILAPNN---
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                                                                                                     SENEY ------TKNDDKYNNSTNSNGY-----NKEIEFLKNIAKEHSLKKIEKN
                                                                                                                                                                                       MI----ESNNDNRNDKNCFKNTNPYNERHIIVDKTNKNGNNNNINSNSNNFDS--ISNI
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                                                                                                                            RLYQIK-----IQYQRENPTEKGLDFK---LYW---TDSQN-----KKEVISSDNL
                                                                                                                                                                     QLPELKOKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDV-KNKRTFLSPWISNI
                                                                                  SENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEV---INKASNSNKIRLEKG
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                                                              275;
                                         Length 3468;
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                                                              Indels
                    506F7D62999BA7B1 CRC64;
                                           DB 5;
                                         5.7%; Score 215.5; DE
19.4%; Pred. No. 0.16;
cive 134; Mismatches 2
EMBL, AE014841, AAN35955.1; -. Hypothetical protein. SEQUENCE 3468 AA; 411913 MW;
                                                     al Similarity 19.4
162; Conservative
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01-OCT-2000 (TEMBLE 15, 01-OCT-2000 (TEMBLE 15, 01-MAR-2003 (TEMBLE 1, 23, Hypothetical protein UV482.

BH HAD

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PRELIMINARY;

Q9PQ08 ID Q9PQ08 AC Q9PQ08;

RESULT 12

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-----NDIIETNVINGSSLVNNDGKTSIRFTLNNLKANKLYSLVDVYYLVNNNSNTIVE 4415
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YQLLLSNINSN------REYRFEKIEINHISNINNFEDLEKLNGVSNTFITQTKNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 LLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELBNIPSENQYFQSAIWSGFIKVKKSDEYT
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Ureaplasma parvum (Ureaplasma urealyticum biotype 1).

Bacteria, Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.

NCBL_TaxID=134821;

[1]

SEQUENCE FROM N.A.

STRAIN=Serovar 3;

MEDLINE=20500219; PubMed=11048724;

Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,

Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                             186;
                                                                                                                                                                                                                                                                                                                                                                                 DB 16; Length 4688;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                       the mucosal pathogen Ureaplasma
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B53ABFAFFEE1997E
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5.4%; Score 202; DB 16; 1
Best Local Similarity 21.3%; Pred. No. 1;
Matches 174; Conservative 131; Mismatches 325;
                                                                                                                                                                                                                                                                 Nature 407:757-762 (2000).
EMBL, AE002145, AAR30894.1, -.
Hypothetical protein; Complete pi
SEQUENCE 4688 AA, 534980 MM,
                                                                                                                                                                                                                     "The complete sequence of urealyticum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLIKYKSSP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 EKWSTASDPYSDF--EKVTGRI-DKNVSPEARHPLVAAYPIVHVDME------NIILS 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -IRLEKGRLY-QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22255705; PubMed=1236864;
Gardner M.J., Hall N., Fung B., White O., Berriman M., Hyman R.W.,
Gardner M.J., Hall N., Fung B., White O., Deulsen I.T., James K
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Sub B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vardya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Fraser C.M., Barrell B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2849;
                                                                                                                                                                                                                                                       Hypothetical protein.
PF11 0392.
Plasmodium falciparum (isolate 3D7).
Blukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the human malaria parasite Plasmodium falciparum.",
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EMBL; AE014841; AAN35975.1; -.
Hypothetical protein.
SEQUENCE 2849 AA; 335916 MW; B5515D173D96B813 CRC64;
                                                                                                                                                                                             Created)
Last sequence update)
Last annotation update)
                         Query Match
5.3%; Score 200.5; DB 5;
Best Local Similarity 20.6%; Pred. No. 0.64;
Matches 170; Conservative 133; Mismatches 334;
717
NDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS
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23,
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01-MAR-2003
                                                                                                                                                                          Q8IHY4;
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                                          2272 NANYFEDIMOLLINHANILANNILASINYI DÖNYLSYNNINCINGNINKÖTCKDIVIGIPNNIN 2331
                                                                                                                                  2332 QNQI-PTI-ELDDTILKAN--DVNLILLNNNNVVNHSVNVEMLNNIQNVNQKLYNDIQENLH 2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDINE-2255705, PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallon S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairland A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
Mcradden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
Fraser C.M., Barrell B.;
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                                                                                                                                                                                                                                                                                                                                                2448 LDKKEINVKNEEINMANSVLEDTNKENEGND------MKDNKNYIINK--ENNVKNND
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNP
                                                                                                     ---TTKPDMTLKEALK
                                                                                                                                                                                                                                                                                                                 578 LDKIKLNAK-----MNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 riasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NYKWNV---YAVTKENT--IINPSENGDISTNGIKKILIFSKKGYE 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AED14825; AAN37143.1; -.
InterPro; IPR000008; C2.
Pfam; PF00168; C2; 5.
SMART; SM00239; C2; 5.
PROSITE; PSS004; C2 5.
SEQUENCE 1904 AA; 224720 NW; AA36470367BDEC41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
-- DOVYGNIATYNFENGRVRVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                     477 WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE-
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Best Local Similarity 19.8%; Pred. No. 0.47;
Matches 174; Conservative 128; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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  435 NYNOFLELEKTKOLRLDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 23, (TrEMBLrel. 23, (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 419:498-511(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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PF14 0530.
Plasmodium falciparum
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1132
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: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         974 SSINANELKANIQWANDYY----ASNIYNNNNNNNNNNNFIISNNI-ISNYNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I SVNDNEYNNSNFTNDMYNNNN------NNNNNNNCNNSSNSNSNSNOVCLYMPNHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 IYIQMNHDQNNAPILQPINNHLAHINDLCYİHSEKNEYTKİSKUNÇOMNİNPQQSNGKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 ------LYWTDSQNK-----KEVISSDNLQLPELKQKSSNSRKKRSTSAGPT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     800 HYKIKEQMNYVQHIPDYEHDNTTNEMINTQNYT-----NINLDPYIMNQNDNNVYLNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 VVTSSTIGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFAISADNHVIMMVDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 QEVINKASNSNK--------IRLEKGRLYQIKIQYQRENPTEKGLDFK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ------VPDRDNDGIP-DSLEVEGYTVDVKNKRTFLSPWISNIHEKKGL----
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     S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243;
           Ralph
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ra. McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis Fraser C.M., Barrell B., "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTF----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF8748D8A051BAD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.2%; Score 197.5; DB 5;
llarity 18.7%; Pred. No. 0.92;
Conservative 138; Mismatches 322;
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1395 NKWHNFINSYFDLNENEKKKKINIF 1419

Search completed: May 3, 2004, 19:40:06 Job time : 37.6261 secs

Aae18289 Bacillus Aae53717 Bacillus Abp71693 B. authra Aar60183 PA(1-725) Aar61289 Bacillus Aae18289 Bacillus Aae18285 Bacillus Aae18285 Bacillus Aae18285 Bacillus Aae18286 Bacillus Aae18287 Bacillus Aae18287 Bacillus Aae07901 C. botuli Aae07901 C. botuli Aae07901 C. botuli Aae07901 C. botuli Aae07907 C. botuli Aae07907 C. botuli Aae07907 C. botuli Aae07907 C. botuli Aae07907 C. botuli Aae07907 C. botuli Aae07908 C. botuli Aae07908 C. botuli Aae07908 C. botuli Aae07908 C. botuli Aae07908 C. botuli Aae07908 C. botuli

us-09-848-909a-16.rag

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Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                           302. .303
/note= "The mutant comprises a deletion amino acids 302-
325 of the D2L2 loop of the wildtype protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to antibacterial agents comprising mutant forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Phe substituted by Ala"
                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Lys substituted by Asp"
                                                                                                                                                                                                                                                                                                                                                                      ..../note= "Wild-type Asp substituted by
                                                                                                                                                                                                                                                      Anthrax PA K397D/D425K/F427A/D2L2 deletion mutant.
                                                                                                                                                                     ALIGNMENTS
              ABP71693
AAR60183
AAR60193
AAE18288
                                                                         AAE18284
AAM50707
AAE07903
                                                                                               AAE07901
AAE07900
AAE07902
                                                          AAE18287
AAE18286
                                                                                                                                                                                                                                                                                                                  Key Location/Qualifiers Misc-difference 302. .303
                                                                                                                                                                                                           AAM51498 standard; protein; 711 AA
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(HARD ) HARVARD COLLEGE
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Anthrax, PA; protective antigen; antibacterial; pore-forming toxin; B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.

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pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51433)
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                                                                                                                                                             Length 711;
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Pred. No. 7.6e-241;
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tive 0;
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM51484-AAM5150), especially mutants in the B molety of the pore-forming binary A-B anthrax toxin, where the B molety is anthrax protective antigen (PA) and using these mutents or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                                                                                                                                                                                                                                                                                                                                                                                                     Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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                                                                                                            note= "The mutant comprises a deletion amino 325 of the D2L2 loop of the wildtype protein"
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Pred. No. 2e-240;
0; Mismatches 1
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                                                                                 Location/Qualifiers
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Conservative 0;
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mutant

deletion

K397D/F427A/D2L2 (first entry)

Anthrax PA

01-FEB-2002

AAM51497;

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protein; 711

AAM51497 standard;

AAM51497

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Gaps

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Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVKQENRILNESESSSQGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                               QRENPTEKGLDFKLYMTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                                                                                                                                                       <u> QRÉNPTEKGLDFKLYMTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN</u>
                                                                                                                                                                                                                                                                                 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                                                                                                                    GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT
                                                                                                                                                                                                                                                                                                                                                   SNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLV
                                                                                                                                                                                                                                                                                                                                                                                                  TKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERR
compositions of them for protecting against Bacillus anthracis infecti
in humans, especially as vaccines. Note: The present sequence is not
given in the specification but is derived from the Bacillus anthracis
wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                                                                                                  EVKQENRILLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKN
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                                                                                  Score 3635; DB 5; Length 7
Pred. No. 5.9e-240;
); Mismatches 2; Indels
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                                                                                                               Conservative
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                                                                Sequence 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acids 302
                                                                                                                                                                                                                              Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
                                                                                                                                                                 QLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSST
                                                                                                                                                                                  EGLLLAIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLAISSLRODGKTFIDFKKYNDK
                                                                               IAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKN
                                                                                                                                        1 A A VN P S D P L E T T K P D M T L K E A L K I A F G F N E P G N L G K D I T E F D F N F D Q O T S O N I K N
                  LGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEK
                                  TKOLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERR
                                                                                                                                                                                                                                                                711
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/note= "The mutant comprises a deletion amino
325 of the D2L2 loop of the wildtype protein"
403
                                                                                                                                                                                                                                                                             LPLYISNPNYKVNVYAVTKENTIINPSENGDISTNGIKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                  LPLYISNPNYKVNVYAVTKENTIINPSENGDISTNGIKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                       711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-MAY-2001; 2001WO-US014372
                                                                                                                                                                                                                                                                                                                                                        standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus anthracis.
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Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anthrax; PA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anthracis.
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420 480 480 540 540 600 600 99 9

600

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1484-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
TKQLRLDTDQVYGNIATYNPENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERR 480
                                                                                                                                                                                                           BGLLLAIDKDIRKILSGYIVBIBDTBGLKBVINDRYDMLNISSLRQDGKTFIDFKKYNDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protecting humans against anthrax using mutant B groups (anthrax
protective antigens) of the pore-forming binary A-B toxin of Bacillus
                                 IAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKN
                                                                   iaavnipsopilettredmilkealkiafgfnepngniqyqgkditefdfnfdqqtsqnikn
                                                                                                                               EGLILNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDK
                                                                                                       QLABINATNI YTVLDKIKLNAKMNI LIRDKRPHYDRNNI AVGADESVVKEAHREVINSST
                                                                                                                                                                                                                                              LPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYEIG 711
                                                                                                                                                                                                                                                                                LPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Wild-type Lys substituted by Asp"
Misc-difference 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Wild-type Asp substituted by
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Misc-difference 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anthrax PA mutant K397D/D425K/F427A
                                                                                                                                                                                                                                                                                                                                                                            AAM51495 standard; protein; 735 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM51484-AAM5150), especially mutants in the B motety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, sepecially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                                               Location/Qualifiers
302. .303
/note= "The mutant comprises a deletion amino acids 302-
32S of the D2L2 loop of the wildtype protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGKNOTLATIKADENQLSQ1LAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVKQENRILINESESSSQGLLGYYFSDINFOAPMVVISSTIGDLSIPSSELENIPSENQYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKATSTSRTHT
                                                                                                                                                                                                                                                                                                                                                                                               Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
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Pred. No. 1.5e-239;
0; Mismatches 3;
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les 708; Conserv
                Bacillus anthracis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 711 AA;
                                                                     Key
Misc-difference
                                                                                                                                                        WO200182788-A2
                                                                                                                                                                                                                                                               04-MAY-2000;
                                                                                                                                                                                                                                                                                                                                   Collier RJ,
                                                                                                                                                                                            08-NOV-2001.
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/note= "Wild-type Lys substituted by Asp" /note= "Wild-type Asp substituted by Lys"

Location/Qualifiers Misc-difference 397

Misc-difference 425

WO200182788-A2

08-NOV-2001

04-MAY-2001; 2001WO-US014372. 04-MAY-2000; 2000US-0201800P.

(HARD) HARVARD COLLEGE

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                                                               1 EVKOENRILINESESSSQGLIGYYFSDINFOAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                            1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                          OSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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                                    24; Gaps
     Length 735;
                                  Indels
 Score 3626; DB 5;
Pred. No. 2.6e-239;
0; Mismatches 0;
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 99.48;
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                             Matches 711; Conservative
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1849-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DGIPDSLEVEGYTVDVKNKRTFLSPMISNIHEKKGLIKYKSSPEKWSTASDPYSDFEKVT 240
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96.6%; Pred. No. 6.6e-239;
live 0; Mismatches 1;
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Best Local Similarity 96.6
Matches 710, Conservative
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                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-017725/02.
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Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein.

Anthrax PA mutant K397D/D425K.

Bacillus anthracis. Synthetic.

01-FEB-2002 (first entry)

AAM51493;

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                                                    576
                                                                                                                               999
 516
                          540
                                                                                                                                                       DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG 696
                                                                                                                                                                              DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
                                                                                                                                                                                                                                                                                                                                                                                                      Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein.
                   LPQIQETTARII FINGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNI
                                                                   541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKKNAKMNILIRDKRFHYDR
                                                                                                                        NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                                 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
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                                                                                                                                                                                                                                                                                                AAM51485 standard; protein; 735
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                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                              Anthrax PA mutant K397D
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus anthracis.
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                                                                                                                                                                                                            QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
                                                                                                                                                                                                                                                                                                                  121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180
                                                                                                                                                                                                                                                                                                                                                       121 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --------3NSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQLLAPNNYYPSKNLAPIA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        577 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 636
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                                                                                                                                                                                                                                                               61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NANIRYVNIGTAPIYNVLPTISLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                                                                                                      1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60
                                                                                                                                                1 EVKQENRILNESESSSQGILGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNREDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                      DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPQIQETTARIIFNGKDLNLVBRRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 LNAQDDFSSTPITMNYNQFLELEXTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
                                                   Gaps
                                                   24;
Length 735;
99.1%; Score 3614; DB 5; Length 7:
llarity 96.5%; Pred. No. 1.7e-238; Indels
Conservative ), Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM51491 standard; protein; 735 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           697 IKKILIFSKKGYEIG 711
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Query Match
Best Local Similarity
Matches 709; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus anthracis.
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989

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS180), especially mutants in the B molety of the pore-forming binary A-B anthrax toxin, where the B molety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1481)
481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                                                                                                                                                                                                                      DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVIKENTIINPSENGDISING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
                                                                    541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                                                                                                 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                         QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                                                                    NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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99.0%; Score 3613; DB 5; Length 735;
Best Local Similarity 96.5%; Pred. No. 2e-238;
Matches 709; Conservative 0; Mismatches 2; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Phe substituted by Ala"
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                                                                                                                                                                                                                                                                                IKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anthrax PA mutant F427A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-017725/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1494-AAMS150), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacilius anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                                                                                                                                                                                                                                                                                                                                  Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Length 735;
                                                 /note= "Wild-type Asp substituted by Lys"
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Pred. No. 2e-238;
0; Mismatches 2
            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page; 77pp; English.
                                                                                                                                                                    04-MAY-2001, 2001WO-US014372
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nes 709; Conservative
                                                                                                                                                                                                                                                                                       Sellman BR;
                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 735 AA;
              Key
Misc-difference
                                                                                         WO200182788-A2
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (FA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DGIPDSLEVEGYTVDVYGNKRTFLSPWISNIHEKKGLTKYKSSPERWFTASDPYSDPEKVT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ÓSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDGEVINKASNSNKIRLEKGRLYQIKIQY 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNAOKDASSTPITMNYNOFLELEKTKOLRLDTDOVYGNIATYNFENGRVRVDTGSNWSEV 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNAQEDFSSTPITMNYNOFLELEKTKOLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480
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                                                                                                                                                                                                                                                     Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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Pred. No. 3.7e-238;
1; Mismatches 2;
                                                                                 04-MAY-2001; 2001WO-US014372.
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Best Local Similarity 96.3:
Matches 708; Conservative
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                                    AVKQENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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            EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                             QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Synthetic.
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                                                                                  DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
                                                                       969
                                                                                                                                                                                                                                                                      ithrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                                                                        DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                              NNIAVGADESVVKEAHREVINSSTEGLLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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                                                                                                                  IKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                     mutant K397Q.
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Misc-difference
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Best Local Simi
Matches 708;
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                                                                                                                                                                                                                                                      Anthrax PA
                                                                                                                                                                                                                                                                                                                   Synthetic.
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EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

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Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                    DGI PDSLEVEGYTYDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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                                             61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Misc-difference 427
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Synthetic.
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WPI; 2002-017725/02.
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les 708; Conserv
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                                                                                                                                                   ainst anthrax using mutant B groups (anthrax of the pore-forming binary A-B toxin of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                              24; Gaps
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                                                                                                                                                                                                                                                                                                                                                                     98.9%; Score 3608; DB 5; 96.3%; Pred. No. 4.4e-238;
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                        04-MAY-2001; 2001WO-US014372
                                                                                                                                                                                                    Claim 4; Page; 77pp; English
                                                 04-MAY-2000; 2000US-0201B00P
                                                                                                                                                 Protecting humans against protective antigens) of th
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                         (HARD ) HARVARD COLLEGE
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                                                                                                   Collier RJ,
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vacchnes. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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577 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSKKKRSTSAGPTVPDRDN
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                                                                                                                   DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                              GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                                                                                 ------SNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
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The sequence encoding the protective antigen of Bacillus anthracis may be used in the construction of a nucleic acid which encodes a fusion protein comprising the anthrax protective antigen binding domain of the native anthrax lethal factor and a sequence encoding an activity inducing domain of a second protein. The fusion proteins are useful for the specific stilling of tumour calls or the killing of calls infected with intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                          Nucleic acid encoding anthrax toxin fusion protein - useful for targetting toxin to specific cells, eg for killing tumour cells or HIV-infected cells.
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Local Similarity 96.3%; Pred. No. 5.1e-238;
les 708; Conservative 0; Mismatches 3; Indels 24
                                                           Nichols PJ;
                                                           Arora N, Singh Y,
                 DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                        Disclosure; Page 81-83; 124pp; English
                                                           Leppla SH, Klimpel K,
                                                                                                 WPI; 1994-279753/34.
N-PSDB; AAQ70180.
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            DMLNISSLRQDGKTFIDFKKYNDKLPLXISNPNYKVAVYAVTKENTIINPSENGDTSTNG 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                                                                                                                                                      Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine.
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98.9%; Score 3607; DB 5;

Best Local Similarity 96.3%; Pred. No. 5.1e-238;

Matches 708; Conservative 0; Mismatches 3;
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                                                                                                                                                                                                                                                          Bacillus anthracis
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                                                         241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                              ----SNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
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completed: May 3, 2004, 19:36:05

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OM protein - protein search, using sw model

Run on:

May 3, 2004, 19:31:43; Search time 14.6056 Seconds

(without alignments)
2513.152 Million cell updates/sec

Title:

US-09-848-909A-16
Sequence:

Scoring table:

LEVKQENRILNESESSSQGLL......TSTNGIKKLLIFSKKGYEIG 711

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched:

389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0

Maximum Match 0%

Maximum Match 0%

Maximum Match 100%

Database:

1: /cgn2_c/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_c/prodata/2/iaa/5B_COMB.pep:*
2: /cgn2_c/prodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LENGTH: 735 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT: Lieppla, Stephen H.
APPLICANT: Xlimpel, Kurt R.
APPLICANT: Xlimpel, Kurt R.
APPLICANT: Alora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMER: US/08/082,849B
FILING DATE: 2-10N-1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Webber, Kenneth A.
NAME: Webber, Kenneth A.
NAME: Webber, Kenneth A.
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Pred. No. 6.2e-261;
0; Mismatches 3;
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Best Local Similarity 96.3%;
Matches 708; Conservative 0
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517 OYOGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKANILIRDKRFHYDR 576
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                                           301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360
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241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
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US-00-021-601-12

Sequence 12, Application US/08021601

Patent No. 5594631

GENERAL INFORMATION:
APPLICANT: Klimpel, Kurt R.
APPLICANT: Michol, Peter J.
APPLICANT: Arora, Naven

TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ALCATED METHODS

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
STREET: 133 Carnegie Way, Suite 400

STREET: Georgia

COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: 19930212
FILING DATE: 19930212
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFIRENCE/DOCKET NUMBER: 1414.057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION TOPORMATION:
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                       DMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 696
                                                                          DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVZAVTKENTIINPSENGDTSTNG 720
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98.9%; Score 3607; DB 5; Length 735;
Best Local Similarity 96.3%; Pred. No. 6.2e-261;
Matches 708; Conservative 0; Mismatches 3; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Leppla, Stephen H.
APPLICANT: Leppla, Kurr R.
APPLICANT: Leppla, Kurr R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Vogendar
APPLICANT: Singh, Vogendar
APPLICANT: Singh, Vogendar
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:

ZIP: 94105
ZIP: 94105
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: BAFENTIN PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: JUNEARION:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRICATION NUMBER: 31.677
REGISTRICATION NUMBER: 31.677
REGISTRICATION NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHRAACTERISTICS:
LENGTH: 735 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application PC/TUS9401624 ; GENERAL INFORMATION:
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                                                                                                                                  Score 3562.5; DB 1;
Pred. No. 1.8e-257;
1; Mismatches 5;
                                                                                                                                    Query Match
Best Local Similarity 95.5%;
Matches 701; Conservative
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
TYPE: AMINO ACID
                                                                ) TOPOLOGY: linear
) MOLECULE TYPE: protein
US-08-021-601-12
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> Sequence 12, Application US/08082849B; Patent No. 5677274 GENERAL INFORMATION; APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen US-08-082-849B-12

and COMPUTER: USB 4

COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: BatentIn Release #1.0, Version #1.30
SUSTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/082,849B
FILING DATE: 25-JUW-1993
CLASSIFICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Kenneth A.
REFERENCE/DOCKET NUMBER: 15.280-161-1
TELECOMMUNICATION INFORMATION:
TELEFHONE: (415) 576-0200
TELEFERA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUIRNE CHARACTERISTICS: APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Pusion Proteins.
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CARSES ...wnsend and Townsend and Crew LLP
T: Two Embarcadero Center, Bighth Floor
San Francisco
California
Y: ne : 903 amino acids amino acid MOLECULE TYPE: protein US-08-082-849B-12 TOPOLOGY: CITY: Sar STATE: Ca LENGTH:

9

Gaps

27;

5; Indels

Length 903;

Gaps 27; Length Query Match
97.7%; Score 3562.5; DB 1; Length
Best Local Similarity 95.5%; Pred. No. 1.8e-257;
Matches 701; Conservative 1; Mismatches 5; Indels

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240 240 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300 300 -----SNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 336 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGINTADTARL 360 420 120 180 120 9 09 121 . QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADBNQLSQILAPNNYYPSKNLAPIA 1 EVKQENRILINESESSSQGLLGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 1 EVKQENKLLNESESSSGGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDBYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 337 61 181 241 301 361 g g ò g à Db ò 셤 δ qq ð 셤 ठे à

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                                           QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                               DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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Patent No. 5677274

GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Limpel, Kurt R.
APPLICANT: Singh, Yogenda.
APPLICANT: Singh, Yogenda.
APPLICANT: Singh, Yogenda.
APPLICANT: NINCOLS, Peter J.
TITLE OF INVENTION: Related Methods
NINMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Franchisc
STATE: California
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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            LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480
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                                                        LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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Sequence 12, Application PC/TUS9401624
Sequence 12, Application:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Vogendra
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STREET: Steuart Street Tower, 20th Floor, One Market
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Best Local Similarity 95.5
Matches 701; Conservative
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61.QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                                        1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPWVVTSSTTGDLGIPSSELENIPSENQYF
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         633 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT
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Pred. No. 9.8e-248;
4; Mismatches 8; Indels 4
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Leppla, Stephen H.
APPLICANT: Leppla, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogenda
APPLICANT: Singh, Yogenda
APPLICANT: Singh, Yogenda
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MEDIUM TYPE: Floppy disk
COMPUTER: ELEM PC compatible
COMPUTER: ELEM PC compatible
COREALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 1993
CLASSIFICATION:
NAME: Weber, Kenneth A.
RESTSENATION:
REFREENCE/POCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       PCT-US94-01624-31; Sequence 31, Application PC/TUS9401624; GENERAL INFORMATION:
                                                                                                                                                                   701 STNGIKKILIFSKKGYEIG 719
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 31
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 94.0%;
Best Local Similarity 91.9%;
Matches 679; Conservative '
                                                                                                                                STNGIKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           719 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein PCT-US94-01624-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 HYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVI 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNREDQSTQNTDSETRTISKNTSTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 KTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 OSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORBNPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS----RKKRSTSAGPTVP 176
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.908/082,849B
FILING DATE: 25-UN-1993
CLASSIFICATION NUMBER: US 08/021,601
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Weber, Kenneth A.
REFERENCE/DOCKET NUMBER: 15280-161-1
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEC ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acid
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94.0%; Score 3430; DB 1;
Best Local Similarity 91.9%; Pred. No. 9.8e-248;
Matches 679; Conservative 4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                   209 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL 268
                                                                                                                                                                                                                                             APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, E. Ernest
APPLICANT: Schneith E.
APPLICANT: Schneits, James
APPLICANT: Loewer, David
APPLICANT: Loewer, David
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 4421 N W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 QENRILINESESSSQGLLGYYYFSDLNFQAPWVVTSSTTGDLSIPSSELEN--IPSENQYFQ
SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%; Score 759; DB 3; Length 881;
llarity 29.7%; Pred. No. 3.5e-48;
Conservative 136; Mismatches 294; Indels 128; Gaps
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MEDIUM TYPE: Floppy disk
COMPUTER: END FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FLING APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780
FLING APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INPORMATION:
NAME: SAliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/POCKET UNMBER: 31,794
REJERPA: 352-375-8800
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LEMGTH: 81 Amino acids
LEMGTH: 81 Amino acids
                                                                                                                                                                RESULT 10
US-08-960-780-32
; Sequence 32, Application US/08960780
; Patent No. 6204435
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TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                             269 irskkgybig 278
                                                                          702 IFSKKGYEIG 711
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ZIP: 32606-6669
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Best Local 3
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Matches
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               TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADENQLSQILAPNNYYPSKNL 392
                                                                                                                                                            393 APIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09273839A
Patent No. 6329156
GENERAL INFORMATION:
APPLICANT: Cirino, Nick M
APPLICANT: Jackson, Paul J
APPLICANT: Jackson, Paul J
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Distruption of Anthrax Toxin Binding to Cell Surface CURRENT Expression Number: US/09/273,839A
CURRENT FILING DATE: 199-03-22
NUMBER OF SEQ ID NOS: 12
SCOTTWARE: Patentin Ver. 2.0
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                                                                                      WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDFLETTKPDMTLKEALKTARGFNEP
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                                                            ----SNSNSSTVAIDHSLSLAGERTWAETMGLNTAD
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ORGANISM: Bacillus anthracis
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Matches 250; Conserv
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2421 N.W. 41st Street, Suite A-1

Gainesville

Floppy disk

COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:

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95 SIRWIGLIQSKETGPFTFNLSEDEQALIEINGKISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                                                                           155 SD--TKFNIDSKTFKELKLFKIDSQNQPQQDELRNPEFNKKESQBFLAKPSKINLFT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 RENPTEKGLD-----PKLYWTDSQNKKEVISSDNLQLPELKQKSS-----N 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTONT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 VRVDIGSNWSEVLPQIQETIARIIFNGKDLNLVERRIAAVNPSDPLETIKPDMTLKEALK 504
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CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRESS: ADDRE
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Patent No. 6242669
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
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US-09-073-898-32
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95 SIRWIGLIQSKETGDFTFNLSEDEQALIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 20.8%; Score 759; DB 3; Length 881;
Best Local Similarity 29.7%; Pred. No. 3.5e-48;
Matches 236; Conservative 136; Mismatches 294; Indels 128; Gaps
COMPUTER: IN FC compatible
COMPUTER: IN FC compatible
COMPUTER: IN FC compatible
COMPUTER: PACEDIA FC-DOS/MS-DOS
SOTTWARE: PACEDIA FC-DOS/MS-DOS
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/073,898
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
ATTORNEY/ABENT INFORMATION:
AMPLICATION NUMBER: US 08/960,780
FILING DATE: APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: APPLICATION NUMBER: US 08/960,780
                                                                                                                                                                                                                                                                                                                                                                             NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-810
TELEPAX: 352-375-800
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE: INDIVIDUAL ISOLATE: PS177C8
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amino acid
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LLNID-----KDIRKILSGYIVEIEDTE-------GLKEVINDRYDMLNI-- 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 TSQFNTASAGYLNANVRYNNVGTGAIYDVKPTTSFVL-NNDTIATITAKSNSTALNISPG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 NYYPSKNLAPIALNAQKDASSTPITMNYNOFLELEKTKQLRLDTDQVYGNIATYNFENGR 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---INTADIARLINANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADENQLSQILAPN 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IAF--GENEPNGNLOYOGKDITEFDF--NFDOOTSONIKNOLAEL-----NATNIYTVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT-STNGIK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIRWIGLIQSKETGDFTFNLSEDEQALIBINGKLISNKGKEKQVVHLEKGKLVPIKIEYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKMKREIDED----TDTDEDEJPLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKNQ---QKEMDRKGLLGYYFKGKDF-SNLTWFAPTRDSTLİYDQQTANKLLDKKQQEYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SD--TKFNIDSKTFKELKLFKIDSQNQPQQDELRNFFFNKKSQGFLAKPSKINLFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 QENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLIKYKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%; Score 759; DB 4;
.larity 29.7%; Pred. No. 3.5e-48;
Conservative 136; Mismatches 294
                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
CRIGINAL SOURCE:
CINDIVIDUAL ISOLATE: PS177C8a
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     699 -KILIFSKKGYEIG 711
                                                                                                                                                                                           881 amino acids
                                                                                             TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 236; Conserv
                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                             US-09-307-106-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            642 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT-STNGIK-- 698
                                                                                                                                                                IAF--GFNEPNGNLOYQGKDITEFDF--NFDQQTSQNIKNQLAEL-----NATNIYTVLD 555
                                                                                                                                                                                                                            LSYPDEIKEIEGLLYYKNKPIYESSVMTYLDENTAKEVTKQLNDTTGKFKDVSHLYDV-- 606
                                                                                                                                                                                                                                                                                                                                                                                                                    604 LLNID-----KDIRKILSGYIVEIEDTE-------GLKEVINDRYDMLNI-- 641
                                           VRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKBALK 504
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APPLICANT: Stamp, Lisa
APPLICANT: Stamp, Lisa
APPLICANT: Stamp, Lisa
APPLICANT: Mortill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: O. 660363el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 241 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTY: Gainesville
STATE: FL
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORPY disk
MEDIUM TYPE: FLORPY disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIKSNPISSIHIKT-NDEITLFWDDISI-TDVASIKPEN--LTDSEIKQIYSRYGIKLE
                                                                                                                                                                                                                                                                                     KIKLNAKMILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG------L
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/960,780 FILING DATE: 30-CCT-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 09/073,898 FILING DATE: 05-MAY-1998 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/307,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Feitelson, Jerald S. Schnepf, H. Ernest Narva, Kenneth E. Stockhoff, Brian A. Schmeits, James Loewer, David Dullum, Charles Joseph Muller Cohn, Judy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
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REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KILIFSKKGYEIG 711
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APPLICANT:
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642 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT-STNGIK-- 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641
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                                                                                                                                                                                                                                                             283 DSETRIISKNISTSRIHISNSNSS-------TVAIDHSLSLAGERIWAEIMG- 327
                                                                                                                                                                                                                                                                                     ---LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPN 384
                                                                                                                                                                                                                                                                                                                                                              385 NYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGR 444
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                                                                                                                                             213 OKMKREIDED----TDTDGDSIPDLWEENGYTI----ONRIAVKWDDSL-ASKGYTKFVSN 264
                                                                                                                                                                                      223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLYAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                               320
                                                                      155 SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPEFNKKESQBFLAKPSKINLFT 212
95 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLBKGKLVPIKIEYQ 154
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                                                                                                                                                                                                              505 IAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL----NATNIYTVLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              556 KIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG------L
                                                                                                             163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHBKKGLTKYKSS
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APPLICANT: Kostichka, N. Kristy
APPLICANT: Estruch, Juan J
TILE OF INVENTION: No. 5770696el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Claba-Gergy Corporation
STREET: 7 Skyline Drive
                                      122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08471033 Patent No. 5770696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
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STATE: NY
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20.8%; Score 759; DB 4; Length 881;
Best Local Similarity 29.7%; Pred. No. 3.5e-48;
Matches 236; Conservative 136; Mismatches 294; Indels 128; Gaps 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAIWSGFIKVXKSDEYTFATSADNHVTWWDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
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INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 QENRILINESESSSOGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFIWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Sanders, Jay M. REGIGINATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
ELING DATE: 30-0CT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
INDIVIDUAL ISOLATE: PS177C8
;
US-09-850-351A-32
                                                                                                                                                      Feitelson, Jerald S. Schnepf, H. Ernest Narva, Kenneth E. Stockhoff, Brian A. Schmeits, James Loewer, David Dullum, Charles Joseph Miller-Cohn, Judy
                                                                                                   Sequence 32, Application US/09850351A
Patent No. 6656908
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 352-375-8100
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TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
          777 DGILIDKKGGIHYG 790
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Morrill, Ge
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                                                                  RESULT 13
US-09-850-351A-32
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552 LSYPDEIKEIBGLLYYKNKFIYESSVMTYLDENTAKEVTKQLNDTTGKFKDVSHLYDV-- 609
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                                                                                                                                                                                                                                                                                                                                                                                                                         664 ILNTDAQEKLNKNRDYYISLYMKSEKNTQCEITIDGEIYPITTKTVNVNKDNYKRLDIIA 723
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APPLICANT: Worlel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Obesi, Wallin M
APPLICANT: Besi, Wallin M
APPLICANT: Bestruch, Wallin M
APPLICANT: Bestruch, Juan J
ITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSED: CIBA-GEIGY / ---
STRREY.
                                                                                                                                                                                                                                                                   610 --KLTPKANVTIK-LSILYDN---AESNDNSIGKWTNTNIVSGGNNGKKQYSSNNPDANL
                                                      IAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL----NATNIYTVLD
                                                                                                                                                                                                            56 KIKLNAKMILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG-----L
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CURRENT APPLICATION DATA:
APPLICATION UNDERS:
FILING DATE:
CLASSIFICATION UNDERS:
CLASSIFICATION UNDERS:
BRIOR APPLICATION UNDERS:
APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
CLING DATE:
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7 Skyline Drive
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08471044; Patent No. 5840868; GENERAL INFORMATION:
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CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 RENPIEKGLD-----FKLYWIDSQNKKEVISSDNLQLPELKQKSS-----N 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
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----NSVESHSSTNWSYINTEGASVEAGIGFKGISFGVSVNYQHSETVAQE--#GTSTGN 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 OKMKREIDED---TDTDGDSIPDLWEENGYTI----ONRIAVKWDDSL-ASKGYTKFVSN 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 NYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGR 444
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Best Local Similarity 29.7%; Pred. No. 5e-48;
Matches 238; Conservative 131; Mismatches 289; Indels 144; Gaps
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CLASSIFICATION DATE:

CLASSIFICATION DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

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ZIP: 10532
MODPUTER READALLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
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JACTERISTICS:
TYPE: amino acids
TOPOLOGY: lift
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Query Match 20.8%; Score 757; DB 2; Length 864;
Best Local Similarity 29.7%; Pred. No. 5e-48;
Matches 238; Conservative 131; Mismatches 289; Indels 144; Gaps 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 ----NSVESHSSTNWSYINIEGASVEAGIGPKGISFGVSVNYQHSETVAQE--WGTSTGN 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          378 TSQFNTASAGYLNANVRYNNVGTGAIYDVKPTTSFVL-NNDTIATITAKSNSTALNISPG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385 NYYPSKULAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437 ESYPKKGQNGIAITSMDFNSHPITLNKKQVDNLLNNKPMMLETNQTDG---VYKIXDTH 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            445 VRVDIGSNWSEVLPQIQETIARIIFNGKDLNLVERRIAAVNPSDPLETIKPDMTLKEALK 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  610 --KLTPKWNVTIK-LSILYDN---ABSNDNSIGKWTNTNIVSGGNNGKKQYSSNNPDANL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 LLNID-----KDIRKILSGYIVEIEDTE------GLKEVINDRYDMLN--- 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT- 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 QKMKKREIDED----TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 DSETRIISKNISISRIHISNSNSS------IVAIDHSLSLAGERIWAEIMG- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADBNQLSQILAPN 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QENRILINESESSSQGILGYYFSDINFQAPMVTSSTTGDLSIPSSELEN--IPSENQYFQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42 QKNQ---QKEMDRKGLLGYYFKGKDF-SNLTMFAPTRDSTLIYDQQTANKLLDKKQQEYQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556 KIKLNAKMILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG-----L
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                                                                                               : 884 amino acids
amino acid
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-044-5
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Sequence 17, Appl Sequence 19, Appl Sequence 20, Appl Sequence 21, Appl Sequence 23, Appl Sequence 7, Appli Sequence 6, Appli Sequence 1, Appli Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 30, Appl Sequence 681, Appl Sequence 681, Appl

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Sequence 30, Application US/10410647

Sequence 30, Application US/10410647

Publication No. US20030235818A1

GENERAL INFORMATION:
APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: Deans, Robert Mary

APPLICANT: Deans, Robert Mary

APPLICANT: Summer, Mary

APPLICANT: Number, Mary

TITLE OF INTENTION: IMMUNGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME

TITLE OF INTENTION: IMMUNGENIC DEALS, 10647

CURRENT APPLICATION NUMBER: US/10/410,647

CURRENT FILING DATE: 2002-04-08

PRIOR PRIOR PLICATION NUMBER: US 60/371,256

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 46

NUMBER OF SEQ ID NOS: 46

SOFTWARRE PATENTIN VETSION 3.1
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APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Tre
TITLE OF INVENTION: and Prevention of Bacterial Infe
FILE REFERENCE: 00742/06002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 736
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Publication No. US20020039588A1
GENERAL INFORMATION:
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TYPE: PRT
; CRGANISM: Bacillus anthracis
US-09-848-909-1
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| Publication No. US20020039588A1
| GENERAL INFORMATION: US20020039588A1
| APPLICANT: COllier, R. John | APPLICANT: Collier, R. John | APPLICANT: Collier, R. John | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: and Prevention of Bacterial Infection | TITLE OF INVENTION: 004204060002 | CURRENT APPLICATION NUMBER: US/09/848,909 | CURRENT FILING DATE: 2001-05-04 | NUMBER OF SEQ ID NOS: 35 | SOFTWARE: FastSEQ for Windows Version 4.0 | SEQ ID NO 2 | LENGTH: 736
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Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Land Prevention of Bacterial Infection
FILE REFERENCE: 00742/60002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
                                                               Indels
                             98.9%; Score 3607; DB 12;
96.3%; Pred. No. 1.2e-262;
iive 0; Mismatches 3;
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PRIOR FILING DATE: 2000-04-04
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                                              Best Local Similarity 96.3°
Matches 708; Conservative
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                                                                                                                                                                                                                                                                        98.9%; Score 3607; DB 12; 96.3%; Pred. No. 1.2e-262;
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, NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 736
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                                                                                                                                  TYPE: PRT ORGANISM: Bacillus anthracis US-09-848-909-3
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Matches 708; Conservative
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TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                           Indels
                                                                                                                                                                                 Score 3607; DB 12;
Pred. No. 1.2e-262;
0; Mismatches 3;
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Best Local Similarity 96.3%;
Matches 708; Conservative
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TYPE: PRT
CRGANISM: Bacillus anthracis
US-09-848-909-4
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RESULT 6 US-09-848-909-5

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| Publication Wo. US20020039588A1
| GENERAL INFORMATION:
| APPLICANT: Collier, R. John
| APPLICANT: Sellman, Brett R.
| TITLE OF INVENTION: Compounds and Methods for the Treatment
| TITLE OF INVENTION: and Prevention of Bacterial Infection
| FILE REPERENT ON/42/060002
| CURRENT APPLICATION NUMBER: US/09/848,909
| CURRENT FILING DATE: 2001-05-04
| PRIOR APPLICATION NUMBER: US 60/201,800
| PRIOR FILING DATE: 2000-04-04
| NUMBER OF SEQ ID NOS: 35
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 5: SEQ ID NOS: 36 Indels Score 3607; DB 12; Pred. No. 1.2e-262; 0; Mismatches 3; Query Match
Best Local Similarity 96.3%;
Matches 708; Conservative IKKILIFSKKGYEIG 711 ; TYPE: PRT ; ORGANISM: Bacillus anthracis US-09-848-909-5 661 697 g

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721 IXXILIFSKKGYEIG 735
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US-09-848-909-7
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                                                                                               Sequence 6, Application US/09848909
; Publication No. US2020039588A1
; Publication No. US202003958BA1
; APPLICANT: Collier, R. John
; APPLICANT: Collier, R. John
; APPLICANT: Collier, R. John
; TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TILE OF INVENTION: and Prevention of Bacterial Infection
; TILE OF INVENTION: 2001-05-04
; CURRENT FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 3607; DB 12; Best Local Similarity 96.3%; Pred. No. 1.2e-262; Matches 708; Conservative 0; Mismatches 3;
721 IKKILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT; ORGANISM: Bacillus anthracis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09848909; Publication VO. US20020039588A1; Sequence 7, Application VO. US2002003958BA1; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Callier, R. John APPLICANT: Callier, R. John TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection FILE OF INVENTION: and Prevention of Bacterial Infection FILE OF INVENTION: AND PROPERTY OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTION OF SECTIO
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Sequence 11, Application US/09848909

Publication No. US20020039588A1

GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
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TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PRESEE for Windows Version 4.0

SEQ ID NO 11

LENGTH: 736
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Pred. No. 1.2e-262;
0; Mismatches 3;
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Best Local Similarity 96.3%;
Matches 708; Conservative
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Publication No. US20202039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
ITILE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
ITILE OF INVENTION: and Prevention of Bacterial Infection
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
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Pred. No. 1.2e-262;
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Best Local Similarity 96.3%;
Matches 708; Conservative
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Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
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 Score 3607; DB 12;
Pred. No. 1.2e-262;
0; Mismatches 3;
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Sequence 16, Application PC/TUS0335733
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE PERBRECE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT RILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGHH: 711
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10 US-09-848-909A-14
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llarity 100.0%; Pred. No. 6.8e-287;
Conservative 0; Mismatches 0;
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ORGANISM: Bacillus anthracis
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                                                              3, 2004, 19:36:13 ; Search time 169.814 Seconds (without alignments) 4086.665 Million cell updates/sec
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3: /cgn2_6/ptodata/2/paa/B007_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/B007_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/B0082_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/B0082_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/B0082_COMB.pep:*

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11: /cgn2_6/ptodata/2/paa/B0082_COMB.pep:*

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13: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*

14: /cgn2_6/ptodata/2/paa/US092_COMB.pep:*

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17: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*

18: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*

19: /cgn2_6/ptodata/2/paa/US094_COMB.pep:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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GENERAL INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

FILE REPERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT FILING DATE: 2001-05-04

PRIOR PRIOR DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 711
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; ORGANISM: Bacillus anthracis
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(GENERAL INFORMATION:
) APPLICANT: President and Fellows of Harvard College et al.
) TITLE OF INVENTION: Compounds and Methods for the Treatment;
) TITLE OF INVENTION: Compounds and Methods for the Treatment;
) TITLE OF INVENTION: Compounds and Methods for the Treatment;
) TITLE OF INVENTION: Compounds and Methods for the Treatment;
) FILE REFERENCE: 0742/072003
(CURRENT PILION DATE: 2003-10-10
) PRIOR PILICATION NUMBER: PCT/US03/35733
(CURRENT FILING DATE: 2002-11-08
) NUMBER OF SEQ ID NOS: 38
) SOFTWARE: FastSEQ for Windows Version 4.0
) SEQ ID NO 15
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No. 2.1e-286;
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENGTH: 711
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      Best Local Similarity 99.9%;
Matches 710; Conservative
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GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REFERENCE: 0742/060002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR PILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 711
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APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT APPLICATION NUMBER: US 60/204
PRIOR PILING DATE: 2001-05-04
PRIOR PELING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
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 Pred. No. 7.7e-286;
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Best Local Similarity
Matches 709; Conserv
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Sequence 12, Application PC/TUS0335733
GENERAL INPORMATION:
FORDILLAMY: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REFERENCE: 0742/072003
CURRENT FILING DATE: 2003-10-10
PRIOR PAPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 711
  Length 711;
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                                      Indels
Score 3635; DB 23;
Pred. No. 7.7e-286;
0; Mismatches 2;
    99.68;
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  Query Match 99.69
Best Local Similarity 99.79
Matches 709; Conservative
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Sequence 12 Application US/09848909A

GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds
TITLE OF INVENTION: Compounds
TITLE OF INVENTION: Compounds
TITLE OF INVENTION: Compounds
TITLE OF INVENTION: 2001-05-04

CURRENT FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PSECSEQ for Windows Version 4.0

SEQ ID NO 12
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     Length 711;
                                  Indels
                                  3,
Score 3629; DB 1;
Pred. No. 2.4e-285;
0; Mismatches 3;
 Query Match
Best Local Similarity 99.6%;
Matches 708; Conservative
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US-09-848-909A-12
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US-09-848-909A-12
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                                                                                                                               1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                             QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Sequence 13, Application PC/TUS0335733

GENERAL INFORMATION:
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: DC 60/424,987
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 735
  Length 711;
                                           Indels
Query Match 99.5%; Score 3629; DB 23; Best Local Similarity 99.6%; Pred. No. 2.4e-285; Matches 708; Conservative 0; Mismatches 3;
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                                                                                                    Score 3626; DB 23;
Pred. No. 4.4e-285;
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                                   TYPE: PRT ORGANISM: Bacillus anthracis
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Matches 711; Conserv
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SEQ ID NO 13
LENGTH: 735
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; Gequence 13, Application US/09848909A
; Gequence 13, Application US/09848909A
; Gequence 13, Application US/09848909A
; APPLICANT: Collier, R. John
; APPLICANT: Callian, Brett R.
; TILLE OF INVENTION: Compounds and Methods for the Treatment
; TILLE OF INVENTION: and Prevention of Bacterial Infection
; TILLE OF INVENTION: and Prevention of Bacterial Infection
; TURENT APPLICATION NUMBER: US/09/848,909A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR APPLICATION NUMBER: US 60/201,800
; RILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
                   735;
                                                     Indels
                   Length
                   Score 3626; DB 1;
Pred. No. 4.4e-285;
); Mismatches 0;
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RESULT 11
PCT-UG03-35733-10
PCT-UG03-35733
Sequence 10, Application PC/TUS0335733
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
APPLICANT: President and Pervention of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REPRESENCE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
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481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKBALKIAFGFNEPNGNL
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   winds and Methods for the Treatment
Prevention of Bacterial Infection
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                                                                                                                                                                                                                                                                          Score 3620; DB 23;
Pred. No. 1.4e-284;
0; Mismatches 1;
TITLE OF INVENTION: Compounds and Methods for TITLE OF INVENTION: and Prevention of Bacter; FILE REFERENCE: 00742/06002 CURRENT APPLICATION NUMBER: US/09/848,909A; CURRENT FILING DATE: 2001-05-04; PRIOR FILING DATE: 2000-06-04; PRIOR FILING DATE: 2000-06-04; NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 10
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Best Local Similarity 96.6%;
Matches 710; Conservative
                                                                                                                                                                                                                      ORGANISM: Bacillus anthracis
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                                                                                                                                                                                   Score 3620; DB 1;
Pred. No. 1.4e-284;
0; Mismatches 1;
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 735
TYPE: PRT
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US-09-846-909A-10
S-09-846-909A-10
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
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Best Local Similarity 96.6%;
Matches 710; Conservative
                                                                                                                           ORGANISM: Bacillus anthracis PCT-US03-35733-10
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                                  Sequence 2. Application PC/TUS0335733
; GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/07203
; CURRENT FILING DATE: 2003-10-10
PRIOR PLLING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                      Length 735;
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Pred. No. 4.2e-284;
0; Mismatches 2;
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Best Local Similarity 96.5%;
Matches 709; Conservative (
                                                                                                                                                                                                                                                            ) TYPE: PRT
; ORGANISM: Bacillus anthracis
PCT-US03-35733-2
                 RESULT 14
PCT-US03-35733-2
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                                                                                                                                                                                                                 ; OTHER INFORMATION: Mature PA sequence including an ETB signal sequence PCT-US03-19786-4
                                                                                                                                                                                                                                                                                                                          EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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                                                and Methods
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99.2%; Score 3617; DB 1; Length 735;
Best Local Similarity 96.5%; Pred. No. 2.4e-284;
Matches 709; Conservative 1; Mismatches 1; Indels 2.
                                                Sequences
                              TILE OF INVENTION: Modified Shine Dalgarno Sec
FILE REFERENCE: PV595PCT
FILE REPERENCE: PV595PCT
CURRENT APPLICATION NUMBER: PCT/US03/19786
CURRENT FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
Sequence 4, Application PC/TUS0319786
GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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RESULT 15
US-09-848-909A-2
is Sequence 2, Application US/09848909A
is GENERAL IMPORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
ITILE OF INVENTION: Compounds and Methods for the Treatment
ITILE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/06002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT PILING DATE: 2001-05-04
FRIOR APPLICATION NUMBER: US 60/201,800
FRIOR APPLICATION NUMBER: US 60/201,800
FRIOR FILING DATE: 2000-05-04
CURRENT PRIDE OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
IENGTH: 735
TYPE: PRT
CORANISM: Bacillus anthracis
US-09-848-909A-2
697 IKKILIFSKKGYEIG 711
721 IKKILIFSKKGYEIG 735
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; DB 23; Length 735; 4.2e-284; hes 2; Indels 24; Gaps 1;	SSELENIPSENOYF		VDDQBVIRKASNSNKIRLEKGRIYQIKIQY 120 	LOLPELKOKSSNSRKKRSTSAGPTVPDRDN 180	LOLPELKOKSSNSRKKRSTSAGPTVPDRDN 180	HEKKGLTKYKSSPEKWSTASDPYSDFEKVT 240	HEKKGLIKYKSSPEKWSTASDPYSDFEKVT 240	LSKONEDOSTONTDSETRISKNISTSRIHT 300	LSKNEDQSTQNTDSETRTISKNTSTSRTHT 300	SNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 336	TVAIDHSLSLAGERTWAETMGLNIADTARL 360	LATIKADENQLSQILAPINYYPSKNLAPIA 396	LATIKADENQLSQILAPNNYYPSKNLAPIA 420	DIDOVYGNIATYNFENGRVRVDTGSNWSEV 456	DIDOVYGNIATYNFENGRVRVDTGSNWSEV 480	SDPLETTKPOMILKEALKIAFGFNEPNGNL 516	SDPLETTKPDMTLKEALKIAFGFNEPNGNL 540	ATNIYTVLDKIKLNAKMILIRDKRFHYDR 576	ATNIYTVLDKIKLNAKMNILIRDKRFHYDR 600	
n Similarity 96.5%; Pred. No. 4.2e-284; 09; Conservative 0; Mismatches 2; Indels	EVKQENRILMESESSSQGLLGYYFSDLNFQAPWVTSSTTGDLSIPS		61 OSAIWGGFIKYKKSDEYTFATSADNHVTMWYDDOEVINKASNSNKTRLEKGRLYOIKTOY 		1. QRENPIEKGLDFKLYWIDSQNKKEVISSDNLQLPELKQKSSNSRKKRGTSAGPTVPDRDN	DGIPDSLEVECYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKW	1 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPY	11 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNT	1 GRIDKOVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT		OI SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL	NANIRYVNIGTAPIYNVLPITSLVLGKNQTLATIKADENQLSQILA	51 NANIRYVNIGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLA	37 INAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNPENGRVRVDTGSNWSEV	21 INAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV	57 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLBTTKFDMTLKEALKIAFGFNEPNGNL	31 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL	7 QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKL	41 QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR	NNIAVGADESVVKEAHREVINSSTEGLLLINIDKDIRKILSGYIVEIED
Query Match Best Local Matches 70		•	اما اما	12;	121	18:	181	24:	241	301	301	33,	36:	9	42:	4.5	48	51,	54.	577
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601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660	637 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKNNVYAVTKENTIINPSENGDTSTNG 696	661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720	697 IKKILIFSKKGYBIG 711	721 IKKILIFSKKGYEIG 735	
Д	ò	d d	δ	Db	

Search completed: May 3, 2004, 19:57:47 Job time : 172.814 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

May 3, 2004, 19:30:47 ; Search time 12.6582 Seconds (without alignments) 5403.004 Million cell updates/sec Run on:

US-09-848-909A-16 3648 1 EVKQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 711 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues

Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		protective antigen	디	cryptic protein -	ical	cal	locat	toxin-like outer m	rhoptry protein -	hypothetical prote	hypothetical prote	rhoptry protein -	_	_	eriz	rai	Ϋ́		hypothetical prote	repeat organellar	cal	hypothetical prote	hypothetical prote	0013	orane nu	E	toxin-like outer m	serine proteinase	oiled coil pro	gen-p
SUMMARIES	ΙD	1 9	75	986	93	10	88	000		367	59	310	367	992	110	703	900	982	53	582	337	53	342	708	134	929	960	187	987	906	867
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	Length		164	875	192	204	68	30	2529	40	752	65	26	7	4919	22	624	36	27	6	8	3216	72	821	1115	12	63	9	769	1208	31
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	Score		3607	849	235.5	35	200	197	192.5	8	190	188	187	187	181	180	79	ത	$\overline{}$	177.5	177	175	-	74	174.5	73	m	m	173	171.5	171
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hypothetical prote hypothetical prote	probable peptidogl	hypothetical prote	probable nuclear p	hypothetical prote	TyB protein - yeas	probable membrane	probable peptidogl	DNA-directed RNA p	ORF MSV156 hypothe	TyB protein - yeas	major merozoite su	hemolysin [importe	TyB protein - yeas	RhoA~binding prote
T18502 T18469	AB1347	T20531	T41023	F82884	852611	E71622	AD1129	T28156	T28317	S31262	SAZQK1	AI0452	S56894	T30868
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171	168	166.5	166	166	165.5	165	165	164	163	163	163	163	163	162.5

ALIGNMENTS

A; Reference number: A59091; MUID:99445483; PMID:105_5943 A; Accession: F99104 A; Accession: F99104 A; Accession: F99104 A; Residuae: 1-313, 'Q', 315-764 < OKI> A; Residuae: 1-313, 'Q', 315-764 < OKI> A; Residuae: 1-313, 'Q', 315-764 < OKI> A; Residuae: 1-313, 'Q', 315-764 < OKI> A; Cross-references: GB:Ar065404; NID:94894216; PIDN:AAD32414.1; PID:94894326 A; Experimental source: strain Sterne A; Brooke: similar to anthrax toxin moiety, protective antigen, pagA formerly pag, plasmid C; Genetics: A; Gene: plasmid C; Genetics: A; Gene: plasmid C; Function: A; Description: three component exotoxin; protective antigen binds to receptors on the symptotic components edema factor or lethal factor; the complex is internalized by receptors components edema factor or lethal factor; the complex is internalized by receptors exotoxin C; Reywords: exotoxin C;

cryptic protein - Bacillus anthracis cryptic protein - Bacillus anthracis C;Species: Bacillus anthracis C;Species: Dacillus anthracis C;Date: 19-0ul-1996 #sequence_revision 19-0ul-1996 #text_change 15-Oct-1999 C;Accession: 139933 R;Welkos, S.L.; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J. Gene 69, 287-300, 1988 A;Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthr A;Reference number: 139933; MUID:89172073; PMID:3148491 A;Recession: 139933 A;Accession: I39933 A;Accession: Light analysis of the GB/EMBL/DDBJ A;Accession: Light analysis of the JNBJ A;Recession: Light analysis of the JNBJ A;Recession: C;Accession: C;

Matches 166; Conservative 127; Mismatches 313; Indels 210; Gaps 37; Conservative 127; Mismatches 313; Indels 210; Gaps 37; Conservative 127; Mismatches 313; Indels 210; Gaps 37; Conservation	180NDGIDEDENGGYIVUNKRETELSPMISNIHEKKGLIKKKSSPEKWSTASDPYSD 3852 IQTQNDTINDTQQTINVTLSGVNSK-YNGRQIKVVYKDNNNVIYESSLITLQKGKND 236 FEKVTGRIDDKVSPEARHPLVAAYPIVHVDMENIILSKN-EDQSTQNTDSET-RTISKNT :::	VRVDIGSNWSEVLPQIQETTARIIFNGKD	OY 627 GLKEVINDRYDMLNISSL-RQDGKIFIDF	RESULT 6 GC6009 SURFACE-Located membrane protein lmp3 precursor - Mycoplasma hominis GC5009 SURFACE-Located membrane protein lmp3 precursor - Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Species: Mycoplasma hominis C;Accession: JC6009 R;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G. J;Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene A;Reference number: JC6009; MUID:96213016; PMID:8631664 A;Accession: JC6009 A;Molecule type: DNA A;Residues: L-1302 <lad> A;Residues: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336 A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64858.1; PID:g1197336</lad>
OY 563 MNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI 622	RESULT 4 G59104 G59104 G59104 C59pechetical protein pXO1-111 - Bacillus anthracis virulence plasmid pXO1 C59peches: Bacillus anthracis C59peches: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000 C5,Accession: G59104 C5,Accession: G59104 C5,Accession: G59104 C7,Aftle: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harboria C5,Aftle: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harboria C5,Catalus: preliminary C5,Catalus: preliminary C5,Catalus: preliminary C5,Catalus: 1-204 <oki>C5,CAS-references: G8:C404, NID:94894216, PIDN:AAD32415.1; PID:94894327 C7,CAS-references: G8:C404, NID:94894216, PIDN:AAD32415.1; PID:94894327 C7,CAS-references: G8:C404, NID:94894216, PIDN:AAD32415.1; PID:94894327 C7,CAS-references: G8:C404, NID:94894216, PIDN:AAD32415.1; PID:94899327 C6,Gentaics: C6,Gentaics: C7,Genta</oki>	Query Match 6.5%; Score 235.5; DB 2; Length 204; Best Local Similarity 34.6%; Pred. No. 3.3e-05; Matches 56; Conservative 36; Mismatches 47; Indels 23; Gaps 6; Qy 563 MNILIRDKREHYDRNIAVGADESVVKEAHREVINSTEGILLANDKDIRKILSGYIVEI 622 Db 1 MNILVRDP-YHYDNGNIAVGADESVVKAAKKQILMWSSDGVSIANDEDRYQALSGYIVEI 622 Qy 623 BDTEGLKEVINDRYDMINISSLRQDGKTFIDFKKYNDKLPLYISNPN 669 Db 60 KKPSNHLINSPVTITLAGKDSGVGELYRVLSDGTGFLDFNKFDENWRSLV-DFG 112 Qy 670 YKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKGYEI 710 LI3 DDVYVAVTKEDFNAVTREDFNAVTREDFNANTABENGNIA-NKLKNTLVLSGKIKEI 153	FB28B5 hypothetical protein UU482 [imported] - Ureaplasma urealyticum C:Species: Ureaplasma urealyticum C:Species: Ureaplasma urealyticum C:Species: Ureaplasma urealyticum C:Accession: F828B5 C;Accession: F828B5 C;Accession: F828B5 C;Accession: F828B5 C:Accession: F828B5 C:Accession: F828B5 C:Accession: F828B5 C:Accession: F82B5 C:Acc	Apparation: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A, Reference number: A82870 A, Reference number: A82870 A, Accession: F82870 A, Molecule type: DNA A, Residuae: 1-4688 cGLA> A, Cross-references: GB. A. E002145; GB. AF222894; NID: G6899476; PIDN: AAF30894.1; GSPDB: GN001 A, Experimental source: serovar 3; biovar 1 A, Experimental source: serovar 3; biovar 1 A, Genetic code: SGC3 A, Genetic code: SGC3 A, Genetic code: SGC3 A, Genetic code: SGC3 A, Charatch Best Local Similarity 20.3%; Pred. No. 0.2;

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C;Superfamily: surface-located membrane protein lmp3; tetratricopeptide repeat homology
C;Reywords: duplication; membrane protein
C;Reywords: duplication; membrane protein
C;Reywords: duplication; membrane protein
E;1-24/Domain: signal sequence #status predicted <MAT>
F;25-1302/Product: surface-located membrane protein Lmp3 #status predicted <MAT>
F;957-992/Domain: tetratricopeptide repeat homology <TT2>
F;1089-1120/Domain: tetratricopeptide repeat homology <TT3>
F;1154-1190/Domain: tetratricopeptide repeat homology <TT4>
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Local Similarity 18.4%; Pred. No. 0.043;
Los 137; Conservative 140; Mismatches 286; Indels 180;
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C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C;Accession: B64635
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Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64635
A;Accession: B64635
A;Accession: Diminary; nucleic acid sequence not shown; translation not shown
A;Accessiones: L-2529 *TOM.
A;Cross-references: GB:AE000602; GB:AE000511; NID:g2314060; PIDN:AAD07969:1; PID:g23140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.3%; Score 192.5; DB 2; Best Local Similarity 20.7%; Pred. No. 0.19; Matches 151; Conservative 95; Mismatches 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              571 RF-----
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T28676 rhoptry protein - Plasmodium yoelii (fragment)	Db 1006 IEKNNKKINABLSNSEKITITQLKENSSLKECQS 1038
C.Species: Plasmodium yoelil C.bate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 01-Dec-2000	QY 631VINDRYDMLNISSLRQDGKTFIDFKKKYNDKLPLYISN-PNYKVNV 674
C.Accession: T28676; A45521 C.Accession: T.K.; KA.; Keen, J.K.; Ogun, S.A.; Holder, A.A. M. Bichka, D. Barait, J. C. 220, 223, 1005	Db 1039 KIKSTIDDNYVSECIKNITNLKTYIVNEKNNINTYFKNAEETVQNVSLNFNNIE 1092
A.Title: Comparison of two members of a multigene family coding for high-molecular mass A.Title: Comparison of two members of a multigene family coding for high-molecular mass A.Reference number: 220507; MUID:97077455; PMID:8920022 A.Accession: T28676 A.Stetus: preliminary; translated from GB/EMBL/DDBJ	OY 675 YAVTKENTIINPSENGDTSTNGIKKLIFSKK 706
A;Notecule type: DNA A;Residues 1-2401 <sin> A;Crose-references: EMBL:U36927; NID:91041784; PID:91041785; PIDN:AAB41263.1 R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.</sin>	RESULT 9 G90599 hypothetical protein MYPU_7030 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
Mol. Biochem. Parasitol. 42, 241-246, 1990 A/Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple cd A/Reference number: A45521, MUID:91101660, PMID:2270106	ext_change 03-Aug-2001
A;Accession: A45521 A;Etatus: preliminary A;Molecule type: DNA A;Residues: 2260-2401 <kee></kee>	R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I. Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul A;Reference number: A99512; MUID:21267165; PMID:11353084
Aftross-references: GB:M34281 Query Match 5.2%; Score 190.5; DB 2; Length 2401; Best Local Similarity 21.6%; Pred. No. 0.22; Matches 176; Conservative 120; Mismatches 321; Indels 197; Gaps 40;	A;Accession: G9U5599 A;Status: preliminary A;Akocaule type: DNA A;Residues: 1-752 <kur> A;Cross-references: GB:AL445566; PID:g14090118; PIDN:CAC13876.1; GSPDB:GN00153</kur>
QY 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSI 45	A,Experimental source: strain UAB Cilp A,Gene: MYPU 7030 A,Genetic code: SGC3
QY 46 PSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEV1 97	Query Match Best Local Similarity 18.7%; Pred. No. 0.043; Matches 152; Conservative 141; Mismatches 258; Indels 260; Gaps 41;
OY 98 NKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELK 157	QY 41 GDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWUD 92
QY 158 QKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSP 205 DD 574 DKLNQNIKTIKETNSIDKIYTDKFENILTDKKTELETKFTGLSLNNHESNNKELLTYFYD 633	Qy 93 DQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQ 140 ::
CY 206 WISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVD 265	Qy 141 NKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTV 194
OY 266 MENIILSKNEDOSTQNTDSETRIISKNTSTSRTHTSNSNSSTVAI-DHSLSLAGERTWAE 324	Qy 195 DVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPY 233
QY 325 TMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKN-OTLATIKAD-ENQLSQI 380	Qy 234 SDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRT 288 :
OY 381LAPNSKNLAPIALNAQKDASSTPITMYNQFLELE 419 DD 779 QIDKLKKVPNKTMFNEDPKEIEKKIENIVEKIDKKKNIYKEIDKLLNEISKIENDKTSLE 838	Qy 289 ISKNISTSRIHISNSSIVAIDHSLSLAGERIWAEIMGLNIADIARLNANIRYVNIGTA 348
QY 420 KTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLN 475	QY 349 PIYNVLPTTSLVLGKRNQTLATIKADENQLSQILAPNNYYPSKNLAP 394
Qy 476 LVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGN 515 i i i i i i i i i i i i i i i i i i	QY 395 IALNAQKDASSTPITWNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTG 450 :: :: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : Db 376 ILTGLKEELSREKLINSIVDKVELKWTSKDAID-KILASTITSKDFDQSQANKRITIGPK 434
QY 516 LQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMILIRDKRFH 573	Qy 451 SNWSEV-LPQIQETTARIIFNGKDLNLVERRIAAV-NPSDPLETTK 494
4 YDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKE 6	495

Cy 278 STQNTDSFTRTISKNTSTSRTHTSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARLN 337	Db 623 LDGSTEKELVPLSTDTTINNSSLGNEDSIYYSLDDADALSENLTD 667	38	668VPLMEIKTTPKYEVVISESVYSSTSYEDNTVAMPPQVEYTSPFMNDPFNSL	384 NNYYPSKNLAPIALNAQKDASSTPLIMNYQFLELEKIKQL	Db 719 NDDYEKKHDLLKSTLAALAPAFTKKDAEFVEAGVTKSCLISTSGHINIFHISKETKQV 776 0v 425 PLDTDOVYGNIATYNFRKGRVEVDTGSNWSEVLPDIOETTAELIFNGKDLNLVERRIAAV 484	777 S-DLDESTENVTFENENTGDENKNOSKNFPGVANSTDKSTEDNTDEKYFSAI	485	828 NYTNVTGDSSCEDIIETASNVEENLKYCEKUNNEAEMSSGDECVKUNDUGSKI	QY 541 QLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHR 593	OY 594 - EVIN	926 AEVVDKLDEEESEDSYEQDYADPEPGNDEGSNENIVKGTKKDTI	Qy 633 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNNYAVTKENTIIN 685	1FS:IMKALSW RESULT 11	rhoptry protein - Plasmodium yoelii C.Species: Plasmodium yoelii	C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_cnange ulrections (C;Accession: T28677; C45521	RyKeen, U.; Sinha, K.; BrOwn, K.; HOLGEr, A. MOl. Blochem. Parasitol. 65, 171-177, 1994 A)Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii A;Reference number: Z20508; MUID:95021522; PMID:7935623	A;Accession: T28677 A;Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA A; Residues: 1-2269 < KBE> A; Cross-references: EMBL: L27838; NID: 9457145; PID: 9457146; PIDN: AAA21304.1	Kikeen, U.; Molder, A.; Flaysall, U.; DOCAYEL, W.; DEWLE, A. Mol. Biochem. Parasitol. 42, 241-25, 1990 A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multipl A;Reference number: A45521; MUID:91101660; PMID:2270106	A, Accession: C45521	A; Molecule type: DNA A; Residues 1211-259 < KEZ>	Query Match 5.1%; Score 187; DB 2; Length 2269; Best Local Similarity 20.5%; Pred. No. 0.31;	; Conservative 119; Mismato	Qy 1 EVKQENKLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSEL 50		9	QY 111 GRLYQIKIQYQRENPT-EKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKRST 169	
Db 495 PDEXMDVBIVKKSSLNQIFVDDFLNTI 521	CY 549 NIYTULDKIKLNAKMILIRDKRFHYDRNNIAVGADESVVK 589	Db 522 NLYKNNTTLSKELRNKRIRQSIEDYFDIKLINFTNSKEYDWRLDFDSNEKAI 573	590 BAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEG-LKEVINDRYDMLNISSLRQDG	Db 574EVKONDNSSSLVFNFKIVKKOVKVHSDKSSGKIEDIVFDKVFSKEVKONLGNAA 626	Qy 649 -KTFIDFKKYNDKLPLYISNPNYKUNVXAVTKENTII 684	685 NPSENGDTSTNGIKKILIFSK 705		RESULT 10	revisiae) othetical protein YM9959	C;Species: SacchaTomyces cerevisiae C;Date: 08-Jul-1995 #sequence_revision 09-Mar-1996 #text_change 29-Oct-1999 C:Brossion: SASIOI: SATARY	R.Dedman, K.; Brown, D.; Bowman, S. submitted to the BMBL Data Library, June 1995	A;Reference number: S55089 A;Accession: S55101 A:Molecule trong. DMA	39934.1; PID:g854471; M	submitted to the BMBL Data Library, June 1995 A, Reference number: 857587	A;Accession: S57587 A;Molecule type: DNA	A;Residues: 608-1658 <ske> A;Cross-references: EMBL:Z49939; NID:g887599; PIDN:CAA90190.1; PID:g887600; MIP A;Experimental source: strain AB972 C;Genetics:</ske>	A, Map position: 13R	Query Match 5.2%; Score 188; DB 2; Length 1658; Best Local Similarity 19.1%; Pred. No. 0.17; Matches 159; Conservative 139; Mismatches 275; Indels 260; Gaps 40;	CY 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSEN 57	OF OVEROSAMINDROTHING CHARACTERS OF THE STATE OF THE STAT	349 FYSEDGAFDEGSVNISVDDSEDDESQAESYSANAENVYHNEHELDDKELIEDIESSDS 40	QY 106 IRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEV 145 : : : : : : : : : : :	of The indictional decay of the control of the indiction of the control of the indiction of the control of the indiction of the control of the indiction of the control of the indiction of the control o	DIIRSSLDKNFHGNNNKSEYSENVLENETDPAIVERENQ-INDVE 51	Qy 191 GYTVDVRUKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASD 231	516 GYDVTGKSVESDLHEHSPDNLYDLAARAMLQFQQSRNSNCPQKEEQVSESYLGHSNGS	OY 232	

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hypothetical protein 2 - Haemophilus ducreyi
C)Species: Haemophilus ducreyi
C)Species: Haemophilus ducreyi
C,Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C,Accession: T31105
R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
A): Bacteriol. 180, 6013-6022, 1998
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Reference number: Z20984; MUID:99030326; PMID:9811662
A;Acteus: preliminary; translated from GB/EMBL/DDBJ
A;Roteus: preliminary; translated from GB/EMBL/DDBJ
A;Roteus: 1-4919 «WAR»
A;Roteus: 1-4919 «WAR»
A;Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
C;Genetics:
A;Genetics:
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                                                SAGPTVPDRDN-----DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPE
                                                                                                                                                225 KWSTASDP-----PLVADFEKVTGRIDKNVSPEARH------PLVAAYPIVHVD
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A;Cross-references: GB:AE001437; PIDN:AAK79054.1; PID:g15023995; GSPDB:GN00168 A;Experimental source: Clostridium acetobutylicum ATCC824 C;Genetics: A;Gene: CAC1080	Query Match 4.9%; Score 180; DB 2; Length 1227; Best Local Similarity 18.8%; Pred. No. 0.28; Matches 164; Conservative 135; Mismatches 273; Indels 300; Gaps	37 SSTIGDLSIPSSELENIPSENQYFQSAIM-SGFIKVKKSDEYTFATSADNHVTM	Db 14 SVTTSAVILSKPAIKAYAADNSVYKSSISNSNEINVKGKEVQEKE	OY 96 V-INKASNSNKIRLEKGRLYQIKIQYQRRNPTEKGLDFKLYWTDSQNKKEVI	Qy 147 SSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTUDVKNYRT	Qy 202 FLSPWISNIHBKKG-LTKYK : : : : : : : : : : : : : :	Qy 221 SSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAA	Qy 259 YPIVHVDMENIILSKNEDQS-TQNTDSETRIISK-NTST 	Qy 296 SRTHISNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNT :	Qy 346 GTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYY	Qy 388 -PSKNLAPIALNAQKDASSTPITWNYNQFLELEKTKQLRLDTDQVYG	OY 434 NIATYNFENGRVRVDTGSNWSEVLPQIQETTARI-IFNGKDLALVERRIAAVNPSDPLET	OY 493 TKPDMTLKEALKIAF-GFNEPNGNLQYQGKDITBFDFNFDQQTSQNIKNO	Qy 542 LAELNATNIYTVLDKIKLNAKOMILIRDKRFHYDRNNI
14 SSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIK 70 :	71 VKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRE 123	SDNLQLPE	342 IKFIVTDKGAGVNHQGVIFAEDDINILTDDGNSRLNKVYADYVRVVGKDIELANNGQIHA 401	156 LKQKSSNSRKKRSTSAGPTVPDRDNDGIPD-SLEVEGYTVDVKNKRTFLSPWISNIHEKK 214	215 GLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHV 264	265 DMENIILSKWEDQSTQNTDSETRTISKNTSTSRTHTSNSNSSTVALDH 312 :: :: : : : : 505NNLKIKKVRDLNLNNSELSANNLTLNTSNNITLKNKSKFTAGNMTLNVTNNVTLNNDS 562	313 SLSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLA 368	369 TIKADENQLSQILAPINYYPSKNIAPIALNAQKDASSTPITMRYNQFLELEKTKQ 423	424 LRLDIDQVYGNIATYNFENGRVRVDTGSNWSBVLPQIQETTARIIFNGKDLNLVERR 480 :	481 I-AAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQCTSQNIK 539 11	540 NQLABLNATNIYTVLDKIKCNAKMNILIRDKRFHYDRNNIA 580	581 VGADESVVKEAHREVINSSTEGLLLNIDKDI 611	612 RKILSGYIVEIEDTEGLKEVINDRYDMLANISSLRQDGKTFIDFKKYNDKLPLY 664 :	665 ISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFSKKG 707

uncharacterized protein, probably surface-located [imported] - Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Species: Clostridium acetobutylicum C;Accession: C97033
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823, 4838, 2001
A;Pitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97033
A;Accession: C97033
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-1227 <KUR>

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N'Alternate names: hypothetical 624 protein; Lmp4 protein
C;Species: Mycoplasma hominis
C;Species: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 11-Jan-2002
C;Accesaion: Dc6003
E;Ladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
J. Bacteriol. 178, 2775-2784, 1996
A;Title: Analysis of 0.5-Kilobase-pair repeats in the Mycoplasma hominis lmp gene system A;Reference number: JG6009; MUD:96213016; PMID:8631664
A;Reference number: JG6009; MUD:96213016; PMID:8631664
A;Residues: 1-624 <LAD>
A;Residues: 1-624 <LAD>
A;Cross-references: EMBL:X95601; NID:g1197335; PIDN:CAA64859.1; PID:g1197337
C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Geneti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 SKNSITNSSNKSDIETANT----ELKQALAKANTDKAQADNLARSTKEQLNKSISSANTL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQST 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 FKLYWTDSQNKKEVISSDNLQLPELKQ-------KSSNSRKKRSTSAGPT- 174
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4.9%; Score 179.5; DB 2; Length 624;
Best Local Similarity 20.8%; Pred. No. 0.11;
Matches 143; Conservative 109; Mismatches 245; Indels 189;
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Search completed: May 3, 2004, 19:41:26 Job time : 15.6582 secs

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OM protein - protein search, using sw model

Run on:

May 3, 2004, 19:27:02 ; Search time 7.98439 Seconds (without alignments) 4636.784 Million cell updates/sec

US-09-848-909A-16 3648 1 EVRQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 711 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

141681

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cription	123	P13422 bacillus an	199	P04932 plasmodium		Q92351 schizosacch	P47024 saccharomyc					Q00798 plasmodium			PO8799 dictyosteli					٠.					P27625 plasmodium					P46082 clostridium	40468	3213 sacch	Q15431 homo sapien
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SUMMARIES	ID	PAG BACAN	YPB1 BACAN	YM67_YEAST	MSP1_PLAFK		PCP1_SCHPO	YJL3 YEAST	RIP3_MOUSE	YFI6_YEAST	RBP2 PLAVB	MDS3 YEAST	RBP1_PLAVB	BXEN_CLOBU	SIR4 YEAST	MYS2 DICDI	USO1_YEAST	S155 YEAST	RIP3_RAT	SPOF SCHPO	CAGA_HELPJ	FAT1_SCHPO	SBCC_LACLA	GLN3_YEAST	RASO_THEVO	RPC1_PLAFA	BEM2_YEAST			BRC2 HUMAN	BXEN CLOBO	TAO3_YEAST		SCP1_HUMAN
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Q07833 bacillus su	P38537 bacillus sp P47037 saccharomvo	Q01550 xenopus lae P54697 dictvosteli	P19321 clostridium O9zkws helicobacte	P08964 saccharomyc	P33968 Baccharomyc P46949 saccharomyc	P25389 saccharomyc
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ALIGNMENTS

EULT 1 - BACAN STANDARD; P13423; Q9FSR7; Q9KH69; Q9F 01-QAN-1990 (Rel. 13, Creat	16-OCT-2001 (Rel. 40, Last sequence update) 10-CT-2003 (Rel. 42, Last annotation update)	Frotective antigen precursor (FA) (FA-03) (FA03) (Antimax translocating protein) [Contains: PA-20 (PA20); PA-63 (PA6	PAGA Bacil	Plasmid pxo1.	Bacteria; Firmicutes; Bacillales; Bacillaceae; NCBI_TaxID=1392;			MEDLINE=891/20/3; Furmed=3140491; Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M.,	Schmidt J.J.;	"Sequence and analysis of the DNA encoding protective antigen	Bacı	[2]			MEDLINE=99214082; Pubmed=10197996; px:cc 1	"Genetic diversity in the protective antique gene of	anthracis.";					Cohen S., Mendelson I., Altboum Z., Kobiler D., Elhanany	Leitner M., Inbar I., Rosenberg H., Gozes Y., Barak R.,	Michael C., Veral B., Sharrerman B., "Attennated recombinant "Attennated recombinant	anthracis spore vaccines protect against anthrax.";				SIKAIN=SCEINE; MEDLINE≈99445483; PubMed=10515943;	Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,	Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter	Martinez Y., Ricke D., Svensson R., Jackson P.J.;	"Sequence and organization of pXOI, the large Bacillus	prasmid marboring the America, coxim T. Bacteriol. 181:6509-6515(1999).			MEDLINE=91332080; PubMed=1651334;	Singh Y., Klimpel K.R., Quinn C.P., Chaudhary V.K., Leppla S	"The carboxyl-terminal end of protective antigen is required		ARRETTER RECEPTER REC	9979.07 (Rel. 13) Cracked 1003 (Rel. 140, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1003 (Rel. 40, Last sequence update) 1004 (Rel. 40, Last sequence update) 1005 (Rel. 40, Last sequence update) 1006 (Rel. 40, Last sequence update) 1007 (Rel. 40, Last sequence update) 1008 (Rel. 40, Rel. 40,
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STRAIN=Weybridge;
MEDLINE=94131936; PubMed=8300513;
KOCHIET T.M., Dai Z., Kaufman-Yarbray M.;
"Regulation of the Bacillus anthracis protective antigen gene: CO2 and a trans-acting element activate transcription from one of two
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MEDLINE=21438996; PubMed=11554763;
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MEDLINE=21092804; PubMed=11178978;
MEDLINE=21092804; PubMed=11178978;
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PROPRIETION OF 148-466 AND PRE-456.

READING STATES OF THE 4-466 AND PRE-456.

READING STATES OF THE 4-466 AND PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-231, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-236; PRE-4511, LEU-232, PRO-234, ILE-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-236, PRE-4511, LEU-232, PRO-234, ILE-232, PRO-234, ILE-232, PRO-234, ILE-232, PRO-234, ILE-232, PRO-234, ILE-232, PRO-234, ILE-232, PRO-234, ILE-2322, PRO-234, ILE-2322, PRO-234, ILE-2322, PRO-234, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE-2322, ILE
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                                   Gaps
                                   24;
   Length 764;
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98.8%; Score 3604; DB 1;
llarity 96.2%; Pred. No. 3.9e-171;
Conservative 1; Mismatches 3;
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STRAIN=S286. / AB972;
MEDLINE=9731368; PubMed=9169872;
MEDLINE=9731368; PubMed=9169872;
MEDLINE=9731088; PubMed=9169872;
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1392;
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P13422; Q9X377;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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17-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
18-OCT-2001 (Rel. 40, Last annotation update)
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[1] SEQUENCE 1

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Chillingworth T.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         623 EDTE------GLKEVINDRYDMLNISSLRODGKTFIDFKKYNDKLPLYISNPN 669
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T -> A (IN REF. 1).
KSCNCILIYVEVSQLANSVFY -> NHVIVYLSM (IN REF. 1).
                                                                                                                                                                    MEDLINE=99445483; PubMed=10515943; Okinaka R.T., Hill K.K., Ckinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K., Cken P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D Martinez Y., Ricke D., Svensson R., Jackson P.J.; Sequence and organization of pXOl, the large Bacillus anthracis Jasmaid harboring the Anthrax toxin genes."; Jasteriol. 181:6509-6515(1999).
                                                        "Sequence and analysis of the DNA encoding protective antigen of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
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003661; Q04988;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical 187.1 kDa protein in GUAl-ERG8 intergenic region.
YMR219W OR YM8261.13 OR YM9959.01.
                    Leppla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.5%; Score 235.5; DB 1; Length Best Local Similarity 34.6%; Pred. No. 2.2e-05; Matches 56; Conservative 36; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670 YKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKGYEI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF. 1).
204 AA; 23029 MW; E1657B23AE4273FD CRC64;
        Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Schmidt J.J.;
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WEDLINE=89172073; PubMed=3148491;
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EMBL; AF065404; AAD32415.1; -.
PIR; 059104; 059104.
PIR; 139933; 139933.
HSSP; P13423; 1ACC.
                                                                               Bacillus anthracis.";
Gene 69:287-300(1988)
                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     349 RYSEDGAFDFGSVNISVDDESEDEESQAESYSANAENVYHHNEHELDDKELIEDIESSDS 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 719 NDDYEKKHDLLKSTLAALAPAF--TKKDAEFVBAGVTKSCLTSTSGHTNIFHTSKETKOV 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-DLDESTENVTFENENTG----DENKNQSKNFPGVANSTDKSTEDNTD----EKYFSAI 827
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Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.; "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.2%; Score 188; DB 1; Length 1658; Best Local Similarity 19.1%; Pred. No. 0.08; Matches 159; Conservative 139; Mismatches 275; Indels 260;
                                                                                                                                                                                                                                                                                          1658 AA; 187137 MW; 3893F968305A757D CRC64;
                                                                                                                                                                                                EMBL; Z49939; CAA90190.1; -...
PIR; S55101; S55101.
Germonline; 1242894; -...
SGD; S0004832; ESCI.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0006548; P:chromatin silencing at telomere; IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     106 IRLEKGRLYQIKIQYQRENPTEKGLDFKL-----
                                                                                                                                                                                      EMBL; Z49809; CAA89934.1; -. EMBL; Z49939; CAA90190.1; -.
                                                               Nature 387:90-93(1997)
                                                                                                                                                                                                                                                                               Hypothetical protein.
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---YKVRNSDLEDDESLKKELTK 925
                                                                                                         926 AEVVDKLDEEESEDSYEQDYADPEPGNDEGSNENIVKGTKK-------DTLGIVEPE 975
                                                    ---SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVI
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                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1987 (Rel. 05, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PMMSA) (P190)
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BAD W., TOOLLE K., BAJBACH H.;
Submitted (JUW-1995) to the EMBL/GenBank/DDBJ databases.
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-!- PTM: Merozoite surface antigen contain the sequence of 83 kDa kDa and 19 kDa antigens which are the major surface antigens merozoites. The maturation take place during schizont.
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InterPro; IPR006219; EGF_like.
Pfam; PF00003; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCB _TaxID=5839;
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881 QISFSTDSPDNFQESNDNTEFSSTK----
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SFTNEVKSKADD-----INSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLKERLFD 1011
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                                                                                                                                64 IWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNS------NKIRLEKGRLY- 114
                                                                                                                                                                                                                                          -----QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                       MENIILSKNEDQSTQNTDSETRTISKNTSTS------RTHTSNSNSSTVAIDHSL 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 SGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVY 675
                                                                                                            ENRL-LNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA
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MSPI PLAFW
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STANDARD; PRT; 1639 AA.

AC P04933;
DT 13-AUG-1997 (Rel. 05, Created)
DT 01-FBB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annocation updace)
DE Merozoite surface protein 1 precursor (Merozoite surface antigens)
DE (PMMSA) (P195).
 1517 1517 N-LINKED (GLCNAC. . .) (POTENTIAL)
1630 AA; 187289 MW; ADBDEC3CE0A46322 CRC64;
                                                                              Indels 263;
                                                   Length 1630;
                                              Query Match
4.8%; Score 173.5; DB 1;
Best Local Similarity 20.6%; Pred. No. 0.41;
Matches 168; Conservative 134; Mismatches 251;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                               [1]
SEQUENCE FROM N.A.
MEDLINE-86014355; PubMed=2995820;
MEDLINE-86014355, TubMed=2995820;
Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 ENRL-LNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA
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                                                                                                                                                                                                                                                                                                 (Potential).
PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
                                                                                                                                                                                                                                                                                    GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MECOZOTE SURFACE PROTEIN 1.

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

N.LINKED (GLCNAC. .) (POTENTIAL).

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N.LINKED (GLCNAC. .) (POTENTIAL).
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PIR; A24594; A24594
PIR; S05603; S05603; S05603; PDB; 1CBJ; 28-MAY-99;
InterPro; IPR006209; EGF_like.
Pfam; PF00008; EGF; 1.
Malaria, Marczoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor; 3D-Emructure.
                                                                                                                                                               "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1639;
                              Plasmodium.
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                                                                                                                                                                                                                                                Holder A.A.;
Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Attached to the membrane by a
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llarity 20.6%; Pred. No. 0.41;
Conservative 134; Mismatches 251;
          Plasmodium falciparum (isolate Wellcome).
Eukaryota, Alveolata, Apicomplexa, Haemosporida,
NCBI_TaxID=5848;
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Best Local Similarity
Matches 168; Conserv
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q	oy d	\$ 8 8	ç q	Qy Gb	6 6	cy Op	Q dd	\$ B	& A	& <u>8</u>	SEAR REFERENCE OCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOOCCOO

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgeon G., RA James M. Gentles S., Horneby T., Hoarin P. S., Horneby T., Hoarin P. S., Horneby T., Hoarin P. S., Horneby T., Jones M., Leather S., McDonald S., Niclean J., Annews M. Jones M., Leather S., McDonald S., Niclean J., Annews M. Jones M., Leather S., McDonay P., Noule S., Marmania M., Marphy L., Mabinowitech E., An Jones M., States S., Sander M., Sharp S., A. Selvon M. S., Marren T., Milechad S., A. Warren T., Milechad S., A. Weller J., Sander J., Sanders M., Scheefer M., Wheller T., Milechad S., A. Weller J., Simmermonia M., Squares M., Scheefer M., Wheller T., Milechad S., A. Gelear J., Cander J., Simmermonia M., Squares M., Scheefer M., Wheller B., Milechad S., An Gooffeau A., Caddeu E., Moler E., Mosel D., Hilbert H., An Borrym K., Langer I., Langer I., Back A., Lehrach H., Schlear M., Wheller B., Moclear G., Jamens S., Xiang Z., Hunt C., Moler E., Moler B., Millardin C., Moler B., Molingar S., Benico J., Moreno S., Amaricog J., Moreno S., Amaricog J., Moreno S., Amaricog J., Moreno S., Amaricog J., Potaburg S., J., Moreno S., Amaricog J., Potaburg S.L., Rochelt M., Gallbart J., Moccandle W.R., Sallsaron J., Moreno S., Amaricog J., Potaburg S.L., Rochelt M., Gallbart G., Schling E., Sallsaron J., Moreno S., Amaricog J., Potaburg S.L., Revuelta S., Revuelta S., Revuelta S., Revuelta S., Marrell B.G., Murse P., Jentled O., Jamens G., Jamens J., Moreno S., Amaricog J., Potaburg S.L., Revuelta S., Revuelta S., Marrell B.G., Murse P., Jentled C., Jamens G., Callone S., Marrell D., G., Murse P., Jentled C., Jamens G., Schlinde Pole body.

It make M., State M., State M., Schlinde Pole body.

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SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222

KNFKLEEKV--DYLSKVND-VEQSQNVKVFTERIR----FLENALEKVQREKDSLSTEME

DSETRIISKUTSTSRTHTSNSNSSTVAI--DHSLSLAGERTWAETWGLNTADTARLNAN-

PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT

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                                                                                                                                                                                                                                                                                                                                             IRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALNA 399
                                                                                                                                                                                                                                  536 IDSITKEKDRLINELEQRIKSYEVNVSELNGT-IDEYRNKLKDKEETYNEVMNAFQYKDN 594
                                                                                                            ERDVLESKL-----QTLE-DDNNSLRLMTSSLGNQIESLRTQNR--EIDEEKNHLRLLAS
                                                                                                                                             460 IQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKBALKIAFGFNEPNGNLQYQ
                                                                                                                                                                                                                                                                                 DLRRFHESINKLQDREKELTSNLEKKNLVISSLRETVAMLEKERESIKKYLSGNAKDLDN
-TLKROIEEKENSSSAFENEENSSYVHLOEDYAILOAKCDEFADRIOVLTADLEKEKENO
                                                       IMHESEASIGLTDSMQVHTLQEQLHKANEEIEFLHDQISRMNEEGKNFEDIMLQFRSLEE
                                                                                    QKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQ
                                                                                                                                                                         ------KNSDKALAETNIRLQEVTKELETLR--MKNSNDLNEIHDLREENBGLTLK
                                                                                                                                                                                                                                                              --KRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKD---IRKILSGYIVEIED
                                                                                                                                                                                                      520 GKDITEFDFNFDQQTSQNIKN---QLABLNATNIYTVLDKIK----LNAKMNIL-IRD-
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MEDLINE=97103775; PubMed=8948101;
MEDLINE=97103775; PubMed=8948101;
MEDLINE=97103775; PubMed=8948101;
Sequencing analysis of a 40.2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2, PST10, GCD14, REIL, PHO86, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon.";
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SGD; S0003649; YJL113W.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00665; rve; 1.
SMART; SM00343; ZnF_C2HC, 1.
Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8B552D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccl
Saccharomycetales, Saccharomycetaceae, Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                   674 VYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYE 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 RYKDIGIHYDRDCNKDKKVIAITDASVGSBYDAQSRIGVILWYGMNIFNVYSNKSTNRCV 1681
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                                                                                             1141 EKENHHPPPIEDIVDM-----SDQTDMESNCQDGNNLKELKVTDKNVPTDNGTNVSPR-- 1193
                     41;
                                                                                                                                                                                                                                            121 QREN----PTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVP 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 TLATIKADENO-----LSQI-LAPNNYYP----SKNLAPIALNAQKDASSTPITM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              411 NYNOFL-ELEKTKOLR-----RUTDOVYGNIATYNFENGRV------RVDTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 NWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNP-SDPLETTKPD-----MTLKEALKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GELNYV-RHKCRYDIEFAVKKVARLVNYPHERVFYMIYKIIQYL-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIRDKRFHYDRN-----NIAVGADESVVKEAHRE----VI-------NSSTEGLL
                                                                 1 EVKQENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                     61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                     ----STNKVE-----KF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              506 AFGFNEPNGNLQYQGKDITEFDFNFDQOTSQNIKNQLAELNATNIYTVLDKIKLNAKMNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INIDKDIRKILSGY---------IVEIEDT----EGLK-----
                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                       177 DRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKK------GLIKY----
                     282;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1742 WIKTEIIKEKIKEKSIKLLKITGKGNIADLLTKPVSASDFKRF 1784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EVINDRYDMLNISSLRQDGKTFI------DFKKY 657
                     262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P3/123,
30-MAY-2000 (Rel. 39, Last sequence update)
30-FEB-2003 (Rel. 41, Last annotation update)
Rho-interacting protein 3 (p116RIP) (RIP3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ā
Best Local Similarity 19.6%; Pred. No. 1.5; Matches 161; Conservative 118; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1024
                                                                                                                                                                                                       -----SNDX-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a placement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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810 EELQSVQRELEVLSEQYSQXCLENAHLAQALBAERQALRQCQRENQELNAHNQELNNRL- 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620 VEIEDTEGLKEVINDRYDMLNI-----SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVN 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGDLSI----PSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEV
504 KIAFGENEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      704 RVALG-REQSAREGYVLQATCERGFAAMBETHQKKIEDLQRQHQRELE-----KLREEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              564 NILIRDKRFHYDRNNIAVGADESVVKEAHRE----VINSSTEGLLLNIDKDIRKILSGYI
                                                                                            ----ERLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETT-
                                                                                                                                                                                                                   ------ARIIFNGKD------LNLVERRI--AAVNPSDPLETTKPDMTLKEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sacchåromyces cerevisiae.";
Nat. Genet. 10:261-268(1995).
-!- SIMILARITY: SOME, TO MANMALIAN NEUROFILAMENT TRIPLET M PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Α.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Hypothetical 137.7 kDa protein in UGSI-PAB1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=S288C / AB972,
MEDLINE=95400292; PubMed=7670463;
MITAKAMI Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                674 VYAVTKENTIINPSENGDISTNGIKKILIFSKKGYEI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           869 AAEITRLRTLLTGDGGGEST--GLP--LTQGKDAYEL 901
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18.9%; Pred. No. 0.98;
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4.5%; Score 102.3; LL.,
Best Local Similarity 18.9%; Pred. No. 0.98;
Matches 151; Conservative 111; Mismatches 253;
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PIR, S56271; S56271.
GermOnline; 140170; -.
SGD; S001912; YFR01GC.
Hypothetical protein.
SEQUENCE 1233 AA; 137697 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
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P43597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNBL outstation the European Bloinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 VTWW---------VDDQEVI--NKASNSNKIRLEKG--RLYQIKIQYQRENPTEK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K--wSTASDP----YSD-FEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451
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                                                                                      MEDINE=97344280, PubMed=9199174;
MEDINE=97344280, Ranenburg O., Poland M., van Horck F.P.G.,
Gebbink M.F.B.G., Kranenburg O., Poland M., van Horck F.P.G.,
Houssa B., Moolenaar W.H.;
"Identification of a novel, putative Rho-specific GDP/GTP exchange
factor and a RhoA-binding protein: control of neuronal morphology.";
J. Cell Biol. 137:1603-1613(1997).
-!- FUNCTION: Rhoa-binding protein involved in control of the actin
cytoskeleton. Overexpression promotes neuronal cell flattening and
neurite outgrowth, probably by counteracting rhoa-mediated
signaling.
-!- TISSUE SPECIFICITY: Highly enriched in the brain.
-!- SIMILARITY: Contains 2 PH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 LLSPPSPSTPHSRRSQVIEKFEALDIEKAEHMETNMLILTTPSSDTRQGRSERRAIPRKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 ANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNYYPSKNLAPIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      225;
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factor, Repeat, Coiled coil.
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116363 MW; A91BDBBB955E45E02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 19.2%; Pred. No. 0.77;
Matches 157; Conservative 131; Mismatches 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.
POLY-SER.
PRO-RICH.
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190
296
976
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185 19
285 29
671 97
1024 AA;
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SEQUENCE
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merozoites."; Cell 69:1213-1226(1992). -!- FUNCTION: Involved in reticulocyte adhesion. Specifically binds to human reticulocyte cells. -!- SUBCELLULAR LOCATION: Membrane-bound (Probable).

structural features with PvRBP-1 and the Plasmodium yoelii 235 rhoptry protein family."; Mol. Biochem. Parasitol. 108:257-262(2000).

SEQUENCE OF 1189-2439 FROM N.A., BEDILINE-29315318; Pubmed-1617731; Medina C.C., Ingravallo P., Barnwell J.W.; Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.; "A reticulocyte-binding protein complex of Plasmodium vivax

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967 SSESSKLSLENIIKNKADLIKKLDQHT--QEIEKHT--FIENEEMSPLLSVIKKEKNRVE 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------MENIILSKWE-DQSTQNTDSETRTISKNTSTSRTHTSNSNSST----VAIDHS 313
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llarity 18.4%; Pred. No. 3.6;
Conservative 147; Mismatches 302; Indels. 268; Gaps
puery Match
Sest Local Similarity
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[1] — SEQUENCE FROM N.A., AND REVISIONS TO 2438-2439.
SEQUENCE FROM N.A., AND REVISIONS TO 2438-2439.
SEQUENCE FROM N.A., PubMed=10838229,
Galinski M.R., Xu M., Barnwell J.W.,
"Plasmodium vivax reticulocyte binding protein-2 (PvRBP-2) shares

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Unpublished observations (XXX-1997).
-!- FUNCTION: NOT KNOWN, NEGATIVE REGULATOR OF EARLY MEIOTIC GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Yeast 13:55-64(1997).
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
MDS3 protein (MCKL dosage suppressor 3).
MDS3 OR YGL197W OR G1307.
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-!- SIMILARITY: TO YEAST YER132C.
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MEDLINE=97197971; PubMed=9046087;
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Matches 171; Conservative 137; Mismatches 271;
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EMBL; 272719; CAA65909.1; -.
PIR; 562048; 562048.
Germonline; 141245; -.
TRANSFAC; T03484; -.
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                                                                   TSRTHTSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYV-----NTGT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fujii N., Kimura K., Yokosawa N., Oguma K., Yashiki T., Takeshi K., Ohyama T., Isogai E., Isogai H.; "Similarity in nucleotide sequence of the gene encoding nontoxic component of botulinum toxin produced by toxigenic Clostridium butyricum strain BL6340 and Clostridium botulinum type E strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium butyricum.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiol. Immunol. 37:395-398(1993).
-!- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Botulinum neurotoxin type E, nontoxic component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1162 AA
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InterPro; IPR008985; ConA_like_lec_gl.
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MEDLINE=93360835; PubMed=8355622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D12739; BAA02231.1;
PIR; I40817; I40817.
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           EMNTYSNSIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                      1306 K----EDDKVTKD-----ISNDKKRNYLPHEKNNLKAKEG--KETRDVREEEEEFDFGLG 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 IPDSLEVEGYTVDVKNXRTFLSPWISNIHE----KKGLTKYKSSPEKWSTASDPYSDFEK 238
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-!- SUBUNIT: Homodimer (Potential).
-!- SUBCELLULAR LOCATION: Membrane-bound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=92315338; PubMed=1617731;
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
"A reticulocyte-binding protein complex of Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                          Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                            MLNISSLRQDGKTFIDFKKYNDKL-PLYISN--PNYKVNVYAVT 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2807 EXTRACELIULAR.
2826 CYTOPLASMIC.
1022 CELL ATTACHMENT SITE
2601 CELL ATTACHMENT SITE
2601 CELL ATTACHMENT SITE
330213 MM; B9DBE442205EBCFF
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9.5%; Pred. No. 3.8;
ve 135; Mismatches 293;
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(Rel. 25, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                    2869 AA
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NCBI_TaxID=31273;
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                                                                  Length 1162;
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                                              C86E9BE932DA78E4
                                                               Query Match
4.4%; Score 159.5; DB 1;
Best Local Similarity 21.5%; Pred. No. 1.3;
Matches 173; Conservative 111; Mismatches 288;
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 Peptidase_M27
InterPro, IPR000395, Peptidase M27
Pfam; PF01742; Peptidase M27, I.
PRINTS; PR00760; BONTOXILYSIN.
ProDom; PD001963; Bontoxilysin, 1.
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                                             136829 MW;
                                              1162 AA;
                                      Neurotoxin
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                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-88142836; PubMed=3325825;
Marshall M., Mahoney D., Rose A., Hicks J.B., Broach J.R.;
Murctional domains of SIR4, a gene required for position effect regulation in Saccharomyces cerevisiae.";
Mol. Cell. Biol. 7:4441-4452(1987).
                                                                                                                                                Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gasser S.M., Cockell M.M.;
"The molecular biology of the SIR proteins.";
Gene 279:1-16 (2001).
-!- FUNCTION: The proteins SIR1 through SIR4 are required for transcriptional repression of the silent mating type loci, M.W. The proteins SIR2 through SIR4 repress multiple loci by modulating chromatin structure. Involves the compaction of chromatin fiber into a more condensed form.
-!- SUBUNIT: Homodimer and interacts with SIR1, SIR2, SIR3 and
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GO, GC:0000783; C:nuclear telomere cap complex; IDA.
GO; GC:0005724; C:nuclear telomeric heterochromatin; IDA.
GO; GC:0006303; P:double-strand break repair via nonhomologou.
Transcription regulation; Repressor; DNA-binding; Nuclear prote
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1358 AA; 152061 MW; 9C698765964F094E CRC64;
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databases.
01-OCT-1989 (Rel. 12, Last sequence update)
28-FEBE-2003 (Rel. 41, Last annotation update)
28-FEBE-2003 (Rel. 41, Last annotation update)
SEGILATOYPY protein SIR4 (Silent information regulator
SIR4 OR STE9 OR ASDI OR UTH2 OR YDR227W OR YD9934.12.
Saccharomyces cerevisiae (Baker's yeast).
Elbarryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomyces.
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ilarity 20.8%; Pred. No. 1.6;
Conservative 113; Mismatches 250;
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SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
Murphy L., Harris D., Barrell B.G., Rajandream Submitted (MAR-1995) to the EMBL/GenBank/DDBJ d
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SEQUENCE FROM N.A.
MEDLINE=95192063; PubMed=7885847;
Davies C.J., Hutchison C.A. III;
"Insertion site specificity of the transposon Nucleic Acids Res. 23:507-514(1995).
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EMBL; U13239; AAC33144.1; -.
EMBL; Z48612; CAA88507.1; -.
PIR; A29360; A29360.
GermOnline; 140719; -.
SGD; S0002635; SIR4.
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105 SKLLSLLRSKTSAGRIESNNPSHDASRSLAS-----FEQTAFSRHAQQQTSTFNSKP 156
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                                                                                                                                                                                                                                          SRST----EKKNDMNISAKNK--NGENKKIGKRPPEIMSTEAHVNKVTEETIKQIQSVR 489
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                                                                               ------GRID-KNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE-
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Gerisch G.;
                                                                                                                                                                                                                                                                                                                          TGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNL
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Bukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
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cad. Sci. U.S.A. 83:9433-9437(1986).
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01-OCT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin II heavy chain, non muscle.
MHCA.
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MEDLINE=90353583; PubMed=2387408;
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                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 1-762.
MEDLINE=95345066; PubMed=7619795;
Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
MEDLINE=98070605; PubMed=9405148;
MEDLINE=98070605; PubMed=9405148;
MEDLINE=98070605; PubMed=9405148;
Maurit C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;
Mayorgetal structure and solution fluorescence characterization of Mg.2'(3')-0-(N-methylanthraniloy!) nucleotides bound to the Dictyostelium missoideum myosin motor domain.";
J. Mol. Biol. 274:394407(1997).
I- FUNCTION: Myosin is a protein that binds to actin and has ATPase activity that is activated by actin.
I- SUBUNIT: Myosin II heavy chain is two-headed. It self-assembles into filaments. Hexamer of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits
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                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment I.,
"X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostellum discoideum myosin motor domain to 1.9-A resolution.";
Biochemistry 35:5404-5417(1996).
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                                                                                                                                                                                                                                                                                                                           of the
                                                            the
PHOSPHORYLATION SITES.
MEDLINE=88112226, PubMed=2828113;
Wagle G., Noegel A., Scheel J., Gerisch G.;
"Phosphorylation of thronine residues on cloned fragments of Dictyostelium myosin heavy chain.";
FEBS Lett. 227:71-75(1988).
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                                                                                                                                                                                               "X-ray structures of the myosin motor domain of Dictyosi discoideum complexed with MgADP.BeFx and MgADP.AlF4-."; Biochemistry 34:8960-8972(1995).
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MEDLINE=97452580; PubMed=9305951;
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
"X-ray structures of the MgADP, MgATPgammaS, and MgAMPP of the Dictyostelium discoideum myosin motor domain.";
Biochemistry 36:11619-11628(1997).
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"X-ray structure of the magnesium(II)-pyrophosphate c
truncated head of Dictyostelium discoideum myosin to
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MEDLINE=95345067; Pubmed=7619796;
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| 494 BIDAANNAKAKAERK--SKELEVRVAELEESLEDKSGTVNVEFIRKKDAEIDDLRARLD- 1550
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Matches 131; Conservative 116; Mismatches 232;
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Plasmid pXO1.
Bacteria; Firmicutes; Bacillales; Bacillaceae;
NCBI_TaxID=1392;
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83363 MW; 292757AD2D5DE5A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                96.9%; Score 3535; DB 2;
llarity 96.0%; Pred. No. 2.8e-160;
Conservative 1; Mismatches 4;
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EMBL, AJ413936, CAC93934.1; -. GO; GO:0005576; C:extraccllular; IEA. GO; GO:0005076; C:extraccllular; IEA. GO; GO:00040821; C:extrachromosomal DNA; IEP. GO; GO:0015070; F:tcxin activity; IEA. GO; GO:009405; P:pathogenesis; IEA. InterPro; IPRO03866; Anthrax toxinB. Ffan; PF03495; Binary toxB; I. PRINTS; PR01391; BINARYTOXINB. NON TER 743 743 743 SEQÜENCE 743 AA; 83363 MW; 292757AD2D5I
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KMNILIRDKRFHY---DRNNIAVGADESVVKEAHREVINSSTEGL------LLINIDK 609
                                                                                                                                                                                                            726 IGSGTTYLDNLSITELNSTPBILDEPEVKIPTDQEIMDAHKIYFADLNFNPS-TGNTYIN 784
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                                           608 GMNILİKTPTYFTNFDDYNNYP--STWSNVNTTNQDGLQGSANKLNGETKIKIPMSELKP
                                                                                                                                                                                 645 RODGKTFIDFKKYND--KLPLYISNPNYKV-----NVYAVTKENTIINPSENGDISTN
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                                                                                       KEVINDRYDMLNIS-SL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CCUG 20309;
Chang S.Y., Song K.P.;
The strain genes of Clostridium difficile strain CCUG 20309.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridia, Clostridiales, Clostridiaceae,
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EMBL; AF211719; AAF81761.1; -.
HSSP; P13423; IACC.
GO; GO:0005576; C:sextracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0019405; P:pathogenesis; IEA.
InterPro; IPR003896; Anthrax toxinB.
Pfam: PF0346; Binary toxB; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.5%; Score 857.5; DB 2;
ilarity 32.0%; Pred. No. 7.1e-33;
Conservative 132; Mismatches 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                        876 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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PRINTS; PR01391; BINARYTOXINB
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01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OT-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Bacteria, Firmicutes,
Clostridium.
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Best Local Similarity
Matches 250; Conserv
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                                                                                     Clostridium difficile.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
Clostridium.
NCBI_TaxID=1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 23.6%; Score 859.5; DB 2; Length 876; Best Local Similarity 32.1%; Pred. No. 5.7e-33; Matches 251; Conservative 131; Mismatches 277; Indels 123;
                                                                                                                                                                                                                                                                  MEDLINE=97230316; PubMed=9119480;

A Perelle S., Gibert M., Bourlioux P., Corthier G., Popoff M.R.;

"Production of a complete binary toxin (actin-specific ADP-ribosyltransferase) by Clostridium difficile CD196.";

Infect Immun. 65:1402-1407(1997).

EMBL; L76081; AAB67305.1; ...

RSP; P13423; 1AC.

GO; GO:001570; F.toxin activity; IEA.

GO; GO:001570; F.toxin activity; IEA.

GO; GO:0015740; F.toxin activity; IEA.

GO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.

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RO; GO:0015740; P.toxin activity; IEA.

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RO; GO:0015740; P.toxin activity; IEA.

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RO; GO:0015740; P.toxin activity; IEA.

RO; GO:0015740; P.toxin activity; IEA.
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                   Last sequence update)
Last annotation update)
  Created)
(TremBLrel. 05, (TremBLrel. 05, (TremBLrel. 24,
                                                                 ADP-ribosyltransferase
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      STRAIN=CD196
                                         01-JUN-2003
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601 EGLLLN------IDKDIRKILSGYIVEIE-DTEGLKEVINDRYDMLNISSLRQDGKT- 650
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                                                                                                                                                                                                                                                                            318 GERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKOOTLATIKADENOL 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 LSSYLESNTAGDPYTDYQKASGSFDKAIKAEARDPLVAAYPVVGVGMEKLIISTNEHAST
                                                                                                                                                                                                                                                                                              374 NGESWNTSLSINKGESAYINANVRYYNTGTAPMYKVTPTTNLVL-DGDTLTTIKAQDNQI
 63 AIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR
                                                                     GNNLSPNETY PKKGLSPLALNTMDQFSSRLIPINYDQLKKLDAGKQIKLETTQVSGN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              547 VLTIGEAIEKAFGATKNGEILYFNGMPIDESCVELIFDGNTANLIKERLNALNDKKIYNV
                206 LKSRSARLASGWGDEDLDTDNDNIPDAYEKNGYTI----KDSIAVKW-EDSFAQQGYKKY
                                                                                                                                                                KSSPEKWSTASDPYSDPEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQST
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                                                                                                          --SRKKRSTSA-GPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKY
                                                      ENPTEKGLDF - - - - - KLYWTDSQNKKEVISSDNLQLPELKQKSSN-
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| : | : | : | : | : | : | KTVSRATINSKIESNIAGVSVNVGYQNGFTANVTINYSHITIDNSTAVQDS---NGE-SWN 376
                                                                                            NNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENG 443
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                                       ETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAP
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STRAIN=CS246;
A Glbert M., Perelle S., Daube G., Popoff M.R.;
Globert M., Perelle S., Daube G., Popoff M.R.;
Globert Bour have a different genomic localization.";
Clostridium spiroforme toxin genes are related to C. perf
toxin genes but have a different genomic localization.";
Syst. Appl. Microbiol. 20:337-347(1997).
SMBL; X97969; CaA66612.1; -.
RSSP; P14242; AACC.
R GO; GO:0015576; C:extracellular; IEA.
R GO; GO:0005976; C:extracellular; IEA.
R GO; GO:0009405; P:pathogenesis; IEA.
R GO; GO:0009405; P:pathogenesis; IEA.
R GO; GO:0009405; P:pathogenesis; IEA.
R PERPPO; IPR003896; Anthrax toxinB.
R PERPPS; PR01319; BINARYTOXINB.
SEQUENCE 879 AA; 98739 MW; 4068SACBBEOSBA01 CRC64;
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Last annotation update)
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Clostridium spiroforme.
Bacteria; Firmicutes; Mollicutes.
NCBI_TaxID=29348;
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01-JUN-2003 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
Sb component.
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lota toxin component Ib precursor.
Clostridium perfrigores.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10ta toxin component 1b precursor.
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STRAIN=NCIB 10748;
MEDLINE=94041637; PubMed=8225592;
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119 -QYQRENPTEKGLD-FKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTV- 175
550 SGETKIIIPMSKLKPYKRYVFSGYSKDPSTSNSITVNIKSKEQKTDYLVPEKDYTKFSYE 709
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
C2 toxin (Component-II).
C3 toxin (Component-II).
C3 toxin (Component-II).
C1 toxin (Somponent-II).
C2 toxin (Component-II).
C1 toxin (Component-II).
C1 toxin (Component-II).
C1 TaxID=1491;
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STRAIN=LYDE C;
MEDLINE=98323874; PubMed=9659689;
Kimura K., Kubota T., Ohishi I., Isogai H., Isogai E., Fujii
Kim etne for component-II of botulinum C2 toxin.";
Vet. Microbiol. 62:27-34(1998).
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21.7%; Score 792; DB 2; Length 721;
Best Local Similarity 34.7%; Pred. No. 7.2e-30;
Matches 218; Conservative 107; Mismatches 222; Indels
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     Perelle S., Gibert M., Boquet P., Popoff M.R.;
Characterization of Clostridium perfringens iota toxin genes and
expression in Escherichia coli.";
Infect. Immun. 61:5147-5156(1993).
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23.3%; Score 849; DB 2; Length 875;
Best Local Similarity 31.3%; Pred. No. 1.8e-32;
Matches 251; Conservative 128; Mismatches 268; Indels 154;
                                                                                                                                                                                                                                                                                                                                        Popoff M.R.;
Submitted (MG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X73562; CAA51960.1;
FIR, 140862; LA4686.2
HSSP; P13423; 1ACC.
GO GO:0005576; C:extracellular; IEA.
GO; GO:0005576; F:exin activity; IEA.
GO; GO:0015070; F:pathogenesis; IEA.
R GO; GO:0015070; F:pathogenesis; IEA.
FEM: PP03495; Binary LoxB; I.R.
FEM: PP03495; Binary LoxB; I.R.
FEM: PRINTS; PR01391; BINARYTOXINB.
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212 875 IOTA TOXIN COMPONENT IB.
875 AA; 98468 MW; C9AE092CD3818921 CRC64;
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                          378 SQILAPNNYYPSKNLAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIAT 437
                                                                                                                                                                                                             GDYLNPGGTYPIIGEPPMALNTMDQFSSRLIPINYNQLKSIDNGGTVMLSTSQFTGNFAX 462
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                                                                                                                                                                                                                                                                                                                                                                                          517 KLTLEQALVKAFALEKKNGKFYFHGLEISKNEKIQVFLDSNTNNDFENQLKNTADKDIME 576
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SEQUENCE FROM N.A.
Shi Y., Chen J., Pang Y.;
Cloning of viplA(C) and vip2A(C) from Bacillus thuringiensis HD201.";
Cloning of viplA(C) and vip2A(C) from Bacillus thuringiensis HD201.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
BMBJ, A7245547, AA086514.1;
GO, GO:0015070; F:toxin activity; IEA.
GO; GO:0005967; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR003995; Anthrax toxinB.
Ffan; PF03495; Binary toxb, I.
PFANTS; PR01391; BINARYTOXINB.
SEQUENCE 775 AA; 87110 MW; 416B2S394361B731 CRC64;
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19.3%; Score 705; DB 2; Length 775;
Best Local Similarity 28.9%; Pred. No. 1.1e-25;
Matches 220; Conservative 129; Mismatches 285; Indels 1:
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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Last sequence update)
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TRTISKNISTSRTHTSNSNSSTVAIDHSLSLAG----
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9 648 545 909 DSETRIISKNISISRIHISNS----NSSTVAID-----HSLSLAGERIWAETMG---- 327 373 NSKSNTEQFNSASAGYLNANVHYNNVGTGGIYDAQPTTSFIL-QDSTIATITAKSNATAL 431 440 FENGRVRVDIGSNWSEVLPQIQETIARIIFNGKDLNLVERRIAAVNPSDPLETIKPDMTL 499 604 607 SAKGLY----DIKLTPKMNITIR-----LATVTLGPDDQFSAYPWENATWSDKFGNLR 655 ------LNIDKDIRK----ILSGYIVE--IEDTEGLKEVI---NDRYDMLNISS 643 PYQAHTVGDPYTDWEKAAGDIPKSNAAATRNPLVAAFPSINVDMRKMILSKDSNLS---- 323 59 GLLLNIDKDIRKILSGYIVEIEDTE------GLKEVINDRYDMLNISSLRQDGNSAEAHSNNSYTYANSEGASIEAGFGPKGFSFGVSANYQHTETVGSDWG -----LNTADTARINANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQ 1LAPNNYYPSKULAPIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYN : : | | | : : | | | | : | : | | | | : | : | | | | : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 542 LAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTE 546 NATNIYTVLDKIKLNAKONILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLL-SECURIOR FROM N.A.
SEQUENCE FROM N.A.
SECURIOR STORE S Query Match

8.1%; Score 296.5; DB 2; Length 225;
Best Local Similarity 37.2%; Pred. No. 5.9e-07;
Matches 68; Conservative 38; Mismatches 54; Indels 23. BXA0163.
Bacillus anthracis.
Plasmid DXOl.
Bacceria; Firmicutes; Bacillales; Bacillaceae; Bacillus. 644 LRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIIN 685 SIFSQNSGGEFKKFTIKTQ-NISG-DYILDSIQLMKRNNDVN 755 225 AA; 25402 MW; 2E121BE54295F9C8 CRC64; RESULT 9
08KYK2
AC 08KYK2,
DF 01-0CT-2002 (TrEMBLrel. 22, Created)
DT 01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
DF 01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
DF Protective antigen-related protein, (pXol-111). 8 8 8 8

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457
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293
                         SUNDESSINIUNNSKNIFVNGNLKISNNLANSGVIEGLELNTNSIENTGNITIKNKLTSQNL 603
                                                                                                                                                                          LPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALN------AQKDASS 405
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                                                                                 STSRIHISNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNV 353
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---ILSKNEDQSTQNTDSETRTISKNT
                                                                                                                                                                                                                                                              406 TPITMNYNQFLELEKTKOLRLDTDQVYGNIATXNFENGRVRVDTGSNWSEV-----L
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Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
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SPRAINE-BASEACHUSETTS / E88;
STRAINE-BASEACHUSETTS / E88;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H. Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H. Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A., Gottschalk G., "The genome sequence of Clostridium tetani, the causative agent tetanus disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

EMBL; AE015938; AA035360.1;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Membrane-associated protein.
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    240 TGRIDKNVSPEARHPLVAAYPIVHVDMEN-
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SEQUENCE 675 AA
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                                                                      60 GVSLNLDEDVNQALSGYMLQIKKPSNHLTNSPVTITLAGKDSGVGELYRVLS-----DG
                                            649 KTFIDFKKYNDKLPLYISNPNYKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKG
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STRAIN=ATCC 25586;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

MEDLINE=21886394; PubMed=11889109;

A Magarral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Wallumas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R., Gensence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586 ","

J. Bacteriol. 184:2005-2018(2002).

EMBL; AE010541; AAL94497.1; EA.

GO: GO: 0008233; P: peptidase activity; IEA.

GO: GO: 0008233; P: peptidase activity; IEA.

GO: GO: 0008233; P: peptidase activity and peptidolysis; IEA.

InterPro: IPR008658; Haemagg_act.

R. InterPro: IPR001452; SH3.
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium
NCFI_TaxID=76856;
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Pfam; PF00018; SH3; 1.
PROSITE; PS00761; SPASE_I_3; 1.
Complete proteome.
SEQUENCE 1881 AA; 204375 MW;
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QBRGK2
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NF-YB.

Plasmodium falciparum.

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5833; 01-MAR-2002 (TrEMBLrel. 20, Created) 01-MAR-2002 (TrEMBLrel. 20, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) CCAAT-box DNA binding protein subunit B. PRT; 1301 AA PRELIMINARY; QBWSK5 RESULT 12

| :: | | | | : | | :: | PIIKKEIKDSENDIREYTFK-------QKBSINLYYVI.PKOVKINBIQLSDSF 617 P--NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDK-IKLN-AKMNILI 567

512

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RDKRFHYDRNNIAVGADESV-----VKEAHREVINSSTEG 602

618

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268

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5.6%; Score 203.5;

Query Match

Length 1301; DB 5;

33, 223 278 246 168 247 KENKENEKNETNEKNATNETNEKNEKNETNETNETNQTNQTNQTNQTNQTNQTNQTNGTN 306 QTNDIVNFDSNKNKPLDEYNHSNIGDCTSVF--KNBINGNYNLEQNMDS----INNVNGV 360 568 630 628 111 TONTDSETRIISKUTSTSRTHTSNSNSSTVAIDHSLSLAGERTWAETMGLN----TADTA 334 RINANIRYVNTGTAPI ----YNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPS 389 ------NQFLELEKTKQLRL 426 484 512 538 IKNOLAELNATNI----YT--VLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEA 591 41 RLYQ---IKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS TSAGPTVPDRD---NDGIPDSLEVE--GYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSP 631 VIND------LRODGKIFIDPKKYNDK SNFSYTNPDKNCNRSNSFTSNIDKESNGNNVNKKSQHVICLNVQNKDHNNNNLKEKEYP 60 FQSAIWSGFIKVKKSDEYTFATSADNHV---TMWVD-----DQEVINKASNSNKIRLEKG EKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHV-----DMENIILSKNEDQS HREVINSSTEGLLL ------NIDKDIRKILSG---YI-----VEIEDTEGLKE 361 AILDAEDMNISKDYDNMNILQNYNMMNNDISFERNLGERMNDKDDRNSYLEDINNKDNYN DIDQVYGNIATYNFE--NGRVRVDIGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAV 485 NPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQG-----KDITEFDFNFDQQTSQN 2 VKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSI -- PSSELENIPSENQY 227; Gaps Indels Best Local Similarity 18.3%; Pred. No. 0.15; Matches 147; Conservative 138; Mismatches 293; ---VSSNPDYLI-----KDNEMIN 702 LPLYISNPNYKVNVYAVTKENTIIN 685 KNLAPIALNAOKDASSTPITMNY----390 112 83 169 143 224 279 335 307 427 466 592 661 42 203 8 & q 8 8 ò g ઠે 셤 à g ∂ g

01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein UU482. Z 4688 PRT; PRELIMINARY; Q9PQ08 RESULT 13

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RESULT 14
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                                Chen E.Y.,
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      STRAIN=Serovar 3;
MEDLINE=20500219; PubMed=11048724;
MEDLINE=20500219; PubMed=11048724;
MEDLINE=20500219; PubMed=11048724;
Glass J. I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen Cassell G.H.;
"The complete sequence of the mucosal pathogen Ureaplasma Trealyticum.";
Interalyticum.";
Nature 407:757-762[2000).
EMBL; AE002145; AAF30894.1; -.
Hypotherical protein; Complete protecome.
SEQUENCE 4688 AA; 534880 MW; BS3ABFRFFEE1997E CRC64;
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                                                                                                                                                                                                                                                                                       MEDINE-2255705; PubMed=12368864;
Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Elsen J.A., Rutherford K., Salberg S.L., Craig A., Kyes S.,
Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S.,
Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
Worfadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Fraser C.M., Barrell B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDIIQERFSHNNIKTYEMNKNCSYDSCDNIVKINYDELNDSTQTKELNEGKSNNGKAEAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - IRLEKGRLY-QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2849;
                                                                                                                                                         Plasmodium falciparum (isolate 3D7).
Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCDI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
5.5%; Score 199.5; DB 5; Length:
Best Local Similarity 20.6%; Pred. No. 0.63;
Matches 169; Conservative 128; Mismatches 322; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE014841; AAN35975.1; -.
Hypothetical protein.
SEQUENCE 2849 AA; 335916 MW; B5515D173D96B813 CRC64;
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                                              Created)
Last sequence update)
Last annotation update)
2849 AA
  PRT;
                                            01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein.
  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falciparum.";
Nature 419:498-511(2002)
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=3D7;
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2337 TI-ELDDTILKNDVNLILNNRVVNHSVNVEMLNNIQNVNQKLYNDIQENLHITNSLH 2393	510 - NEPNGNLOYQGKDITBEDFNFDQQTSQNIKNQLAELNATNIYTVLDKI	2394 NANANANANAMEGGDVEANSYEFNINSFNPARAYIYANANANANANANANANANANANELOKKEI 2453	260	2454 NVKNEEINMÄSVLEDTNKENEGNDMKDNKNYIINKENNVKNNDN	615 LSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNV 674	2503 SNGQNINNTNANTMKEKRNNNLRDDDİYKKNMKRSNSLDFKKLDSEKKNKS	675YAVTKENTIINPSEN	2557 EEGARKWKTNTTQLLNYSENRKKGLRDMSTYADKVLE 2593	11.0	TIO4	Q811104; 0311104; 01.1MP-2002 / MYEMBI - 02	01-MAN-2003 (TIEMULEL 23, Leguence update) 01-MAD-2003 (THEMBLEL) 23, last sequence update) 01-MAD-2003 (THEMBLE) 23 last sequence update)	Hypothetical protein.	Plantonium falciparum (isolate 3D7). Plantonium falciparum (isolate 3D7). Bukarunta: Bluenlata: Bukommulara: Haemnennrida: Plaemndium	NCBL TaxID=36329;				Eisen J. Chan M Pertea Martin D McFadder Venter J	"Genome seque falciparum.", Nature 419:44 EMBL; AE0148 Hypothetical SEQUENCE 3,	Query Match Best Local Similarity 19.0%; Pred. No. 0.81; Matches 157; Conservative 130; Mismatches 263; Indels 275; Gaps 39;	55 SENQYFOSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKG 111	112 RLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKKEVISSDNL 151	152 QLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDV-KNKRTFLSPWISNI 210 15	211 HEKKGLIKYKSSPEKWSTASDPYSDFE-KVTGRIDKNVSPEARHPLVAAYPIVHV- 264 316 NKKISYPINMYSNSEDKTINOINIDMSTLSSPSIKNAYSFYSIS 360	265DMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHTSNSNS
검	ò	QC	δ	Б	ò	g	ò	d	þ	4 Q t	145	555	386	989	õõ	2 2 2	1 2 2 E	2 2 2	* * * * * * * *	8 5 5 5 5 8 5 8 5 8 5 8 5 8 5 8 5 8 5 8		상 점	\$ B	۲۶ d	95 Pb	ò

eted: May 3, 2004, 19:40:09 6.4955 secs

us-09-848-909a-13.rai

120 120 176 180 236 9 9 1 EVKQENRILINESESSSQGLLGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKLQY 177 DRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDF DRDNDG1PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDP 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS----RKKRSTSAGPTVP 61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 24; Length 719; Indels COUNTRY: USA
ZIF: 94105
ZIF: 94105
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patent PC-DOS/MS-DOS
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent NR-Bease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: Unne 25, 1993
CLEASTFICATION:
NAME: Weber, Kenneth A.
REGISTRATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 15280-115
TELEPHONE: (415) 543-500
TELEPHONE: (415) 543-500
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 maino acids
TYPE: amino acids
TYPE: AMINO acids Score 3576; DB 5; Pred. No. 3.8e-249; 4; Mismatches 8; Query Match
Best Local Similarity 95.1%;
Matches 703; Conservative 4 TOPOLOGY: linear MOLECULE TYPE: protein PCT-US94-01624-31 g qq ठ ద ò ò

> 416 420 476

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RIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSSIVAIDHSLSLAGERIWAETMGLNTAD 356

297 301 357

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RIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNL APIALNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN 421 APIALNAQDDFSSTPITMN--------YGNIATYNFENGRVRVDTGSN 460

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WSEVLPOIQETTARIIFNGKDIALVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP NGNLQYQCKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRF NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMILIRDKRF

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HYDRINI AVGADESVVKEAHREVINSSTEGLLLINI DKDIRKILSGYIVEI EDTEGLKEVI

HYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVI

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241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSSTRTISKNTSTSRTHT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPQIQETTARIIFNGKOLNLVERRIAAVNPSOPLETTKPDMTLKEALKIAFGFNEPNGNL
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1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                             181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLIKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYQGKDITEFDFNFDQQTSQNIXQQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
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                                                                                                                                             121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                                                                                 121 QRENPIEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                                                                                                                                            DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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; Sequence 31, Application US/08082849B
; Patent No. 567274
; GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Nichols, Peter U.
TITLE OF INVENTION: Authrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                              QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 600
                                                                                                                                                                                                                                            NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660
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                                                   540
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                                                                                                                                                                                                                                                                                                                                           DMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG 720
  LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Limpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
IILE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: San Francisco
STREET: Steuart Street Tower, 20th Floor, One Market
CONNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATION STREET: PerentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
ATTORREYAGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION POR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TENDHONE: GENERAL STACES:
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Pred. No. 1.5e-258;
1; Mismatches 5;
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FORTURE 94-102
Sequence 12, Application PC/TUS9401624
GENERAL INFORMATION:
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Best Local Similarity 98.8%;
Matches 725; Conservative
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and

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APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: USA
                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-UNN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                            PULDEADLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-193
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REPERENCE/DOCKET NUMBER: 31,677
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
TYPE: amino acid
                                                                                                                                                                                                 ZIP: 94111.3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-08-082-849B-12
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MOLECULE TYPE
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                                                                                                                                                Query Match 98.3%; Score 3708.5; DB 1; Length 903; Best Local Similarity 98.8%; Pred. No. 1.5e-258; Matches 725; Conservative 1; Mismatches 5; Indels 3;
   INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
TYPE: AMINO ACID
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                                                                      TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-021-601-12
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                                                                                                                                         1 EVKQENRILINESESSSQGLIGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENQYF
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                                                                                                   1 EVKQENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
  98.3%; Score 3708.5; DB 1; Length 903; 98.8%; Pred. No. 1.5e-258; ive 1; Mismatches 5; Indels 3;
Query Match
Best Local Similarity 98.8
Matches 725; Conservative
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Sequence 12, Application US/08082849B Patent No. 5677274 GENERAL INFORMATION: APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen

RESULT 5 US-08-082-849B-12

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                               241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300
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                                                                                                                   GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
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                                                                                                                                                                                                               361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC-COMPATIBLE
CONFINING SYSTEM: PC-DCS/MS-DCS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE: 19930212
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 36,016
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPRAK: 404/688-9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 559451

Patent No. 559451

CENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Minpel, Kurt R.

APPLICANT: Michols, Peter J.

APPLICANT: Arora, Naveen

APPLICANT: Arora, Naveen

APPLICANT: Arora, Naveen

TITLE OF INVENTION: RELATED METHODS

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Needle & Rosenberg, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: JOURESS: STREET, P.C. STREET: 113 Carnegie Way, Suite 400 CITY: Atlanta CTTY: Georgia COUNTRY: USA ZID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-021-601-12
Sequence 12, Application US/08021601
Patent No. 5591631
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                                                                              Sequence 4, Application PC/TUS9401624

Sequence 4, Application PC/TUS9401624

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Klimpel, Kurt R.

APPLICANT: Arora, Naveen

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

APPLICANT: Singh, Yogendra

CORRESPONDENCE: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW

STREET: Steuart Street Tower, 20th Floor, One Market

STREET: San Francisco

CITY: San Francisco

COUNTRY: USA

ZIP.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATRE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-BOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3753; DB 5;
Pred. No. 7.2e-262;
0; Mismatches 3;
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NAME: Weber, Kenneth A.
REGISTATION NUMBER: 31,677
REPERENCE/DOCKET NUMBER: 15280
TELEPHONE: (415) 543-9600
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TYPE: amino acids
                                                                                                                      Query Match
Best Local Similarity 99.6%;
Matches 732; Conservative
                                                                                      721 IKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.5%; Score 3753; DB 1; ilarity 99.6%; Pred. No. 7.2e-262; Conservative 0; Mismatches 3;
                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-UNN-1993
CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION HORRE: US 08/021,601
APPLICATION NUMBER: US 08/021,601
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 735 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
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Best Local Similarity
Matches 732; Conserv
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Patent No. 5677274
GENERAL INFORMATION
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APPLICANT: Leppla, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Michols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Ralated Methods
ITLE OF INVENTION: Ralated Methods
CORRESPONDENCE ADDRESS: 35
CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP
CITY: San Francisco
CITY: San Francisco
CITY: San Francisco
STARE: California
COUNTRY: USA
ZIARE: CALIFORNIA
ZIARE COMPURE READABLE FORM:
MEDIUM TYPE: Floppy disk
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2513.152 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-08-849B-4
US-08-01-611-12
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US-08-08-2849B-12
US-08-08-2849B-31
US-08-08-289B-31
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US-08-471-046A-23
US-08-470-566B-23
US-08-469-334-23
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Listing first 45 summaries
                                                                                                        protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCRMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Nichols, Perer J.
APPLICANT: Nichols, Perer J.
APPLICANT: Nichols, Perer J.
APPLICANT: Singh, Yogendra
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
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TITLE OF INVENTION: ANTHRAX TOXIN FUSION
STREET: Jagana Carnegie Way, Suite 400
CITY: Aclanta
COUNTRY: USA
ZIR: Georgia
COMPUTRY: USA
ZIR: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
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COMPUTER: Floppy disk
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,601
FILING DATE: 19930012
CLASSIFICATION: 514
ATTOWNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 1414.057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 4:
SEQUENCE CHRAACTERISTICS:
LENGTH: 735 amino acids
US-08-471-033-36
US-08-471-044-36
US-08-471-046A-36
US-08-471-046A-36
US-08-471-046A-36
US-08-471-033-50
US-08-471-033-50
US-08-471-045A-50
US-08-471-046A-50
US-08-471-046A-50
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US-08-471-046A-50
US-08-471-046A-50
US-08-09-334-50
US-08-09-334-50
US-08-09-311-913A-7
US-09-371-913A-7
US-09-371-913A-7
US-09-371-913A-7
US-09-371-0133-21
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Best Local Similarity 99.6'
Matches 732; Conservative
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                  DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
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DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                                                                                                                                                                                                                                                                                       protein; protective antigen; PA; MAT-PA; TPA-PA; activator; PA63; vaccine; anthrax; antibacterial
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tissue plasminogen
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Search completed: May 3, 2004, 19:36:03 Job time : 52.1208 secs
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS184-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                                                                        Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
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g ö ઠ 음 음 8 The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483) 300 420 420 480 480 600 240 360 540 900 099 120 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 180 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720 9 EVKQENRLINESESSSQGLLGYYFSDLNFQAPWVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKRRSTSAGPTVPDRDN DGI PDSLEVEGYTVDVKMKRTFLSPWI SNI HEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKOVSPEARHPLVAAYPIVHVDMENIILSKOEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQADFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLMAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis. 1 BVKQENRLLMESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA LNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGXDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILLSGYIVEIEDTEGLKEVINDRY Gaps . 0 Length 735; 3; Indels Query Match
99.5%; Score 3753; DB 5;
Best Local Similarity 99.6%; Pred. No. 1.6e-247;
Matches 732; Conservative 0; Mismatches 3; Claim 4; Page; 77pp; English (HARD) HARVARD COLLEGE Sellman WPI; 2002-017725/02 Sequence 735 AA; RJ, 61 241 301 301 361 361 421 421 541 601 61 121 181 181 241 481 501 561 g ઠે 셤 ò g g à g ò 셤 à 셤 8 g δ g à ò δ

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1801), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uthrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVKQENRLINESESSSQGLIGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Asp substituted by Lys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Wild-type Lys substituted by 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Wild-type Lys substituted by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anthrax PA mutant K395D/K397D/D425K/D426K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Wild-type Asp
Misc-difference 426
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                                                                                                                                                                                                                                                                                                  AAM51494 standard; protein; 735
                                                                   735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000; 2000US-0201800P
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                             721 IKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sellman
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Misc-difference 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus anthracis.
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541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 600 601 NNIAYGADESYVKEAHRZVINSSTEGLLINIDKDIRKILSGYIVBIEDTEGLKEVINDRY 660	OY 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180
601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660	QY 181 DGIPDSLEVEGYTVDVRXRRTFLSPWISNIHEKKGLTKYXSSPEKWSTASDPYSDFEKVT 240
661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720 	Db 181 DGIPDSLEVEGYTVDVRNRTFLSPWISNIHEKKGLITKYKSSPEKWSTASDPYSDFEKVT 240 Qy 241 GRIDKAVYSPEARHPLVAAYPIVHVDMENIILSKWEDQSTQNTDSETRTISKNISTSRTHT 300
721 IKKILIFSKKGYEIG 735	Db 241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSIQNIDSETRIISKNTSTSRTHT 300
721 IKKILIFSKKGYEIG 735	CY 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360
RESULT 11 AAM51483 ID AAM51483 standard; protein; 735 AA.	361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA
AAM51483;	361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA
01-PSB-2002 (first entry)	Qy 421-LIARQKDASSTPITMNYNOFLELEKTKOLRLDTDQYYGNIATYNFRIGRYRYDTGSRWSEV 480
Anthrax PA protein.	*** I DNAQDDFOSTFIIMINGFUBLBAIAQDKUDIDQVIGNIALINFENGKVKVDIGSNASEV
Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine.	Db 491 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEBDNGNL 540
Bacillus anthracis.	Qy S41 QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKANILIRDKRFHYDR 600
WO200182788-A2.	Db 541 QYGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKNNILIRDKRFHYDR 600
08-NOV-2001.	Qy 601 NNIAVGADESVVKEAHREVINSSTEGLLLUNDKDIRKILSGYIVELEDTEGLKEVINDRY 660
04-MAY-2001; 2001WO-US014372.	Db 601 NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660
04-MAY-2000; 2000US-0201800P.	Qy 661 DMLNISSLRQDGXTFIDFKKYNDKLPLYISNPNYKNNYAVTKENTIINPSENGDTSTNG 720
(HARD) HARVARD COLLEGE.	Db 661 DMLNISSLRQDGXTFIDFXKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
Collier RJ, Sellman BR;	Qy 721 IKKILIFSKKGYEIG 735
WPI; 2002-017725/02. N-PSDB; AAI99904.	Db 721 IKKILIFSKKGYEIG 735
Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.	RESULT 12 AAM51488 ID AAM51488 standard; protein; 735 AA.
Disclosure, Fig 13, 77pp, English.	AC AAMS1488;
e invention relates to antibacterial agents comprising mutant forms of re-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants the B moiety of the pore-forming binary A-B anthrax foxing where the B	DT 01-FEB-2002 (first entry) XX DE Anthray Da mintant D40sa
moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. The present sequence is that of the	ax, Prety; P
anthrax PA protein	XX OS Bacillus anthracis.
	XX XX
1 EVKQENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60	182788-A2.
QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDGEVINKASNSNKIRLEKGRLYOV	XX XX 04-WAY-2001: 2001WO-US014372.
	X-2000; 2000US-0201

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The sequence encoding the protective antigen of Bacillus anthracis may be used in the construction of a nucleic acid which encodes a fusion protein comprising the anthrax protective antigen binding domain of the native anthrax lethal factor and a sequence encoding an activity inducing domain of a second protein. The fusion proteins are useful for the specific filling of tumour cells or the killing of cells infected with intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                  Mucleic acid encoding anthrax toxin fusion protein - useful for targetting toxin to specific cells, eg for killing tumour cells or HIV-infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
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                                                                    93US-00021601.
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                                         EVKQENRLILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                                                                      DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                         QSA1WSGF1KVKKSDEYTFATSADNHVTMWVDDQEV1NKASNSNK1RLEKGRLYQ1K1QY
                                                                                                                           QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anthrax, Bacillus anthracis, fusion protein, protective antigen, protective antigen, cell killing, targetting, targeting, pathogen; intracellular, HIV, human immunodeficiency virus, toxin.
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS113 and AAMS1800), especially mutants in the B.moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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    81 LPOIGETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                                                                                                                                                                            DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                               QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                                                                  NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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Misc-difference 425
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Matches 732; Conservative
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Misc-difference
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                                                                                                                                                                                                                                                                                                                             nthrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                        QYQGKDITBFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                  QYQGKDITEFDFNFDQQTSQNIKNQLABINATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                                                      NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIBDTEGLKEVINDRY
                                                                                                                                  DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                               EVKQENRILINESESSSQGILGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                   QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                    QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Synthetic.
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vacines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                                                                                                                                                                                                                                                      Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 735;
                                         Location/Qualifiers
425
/note= "Wild-type Asp substituted
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99.5%; Score 3755; DB 5;
Best Local Similarity 99.6%; Pred. No. 1.2e-247;
Matches 732; Conservative 1; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page; 77pp; English!
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                                                                                                                                                                                                                                             Sellman BR;
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   anthracis.
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Misc-difference
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 Bacillus ar
Synthetic.
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM5113 and AAM51464-AAM510), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483) ithrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein. Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis. /note= "Wild-type Asp substituted by Lys" Mey Location/Qualifiers Misc-difference 425 04-MAY-2001; 2001WO-US014372 04-MAY-2000; 2000US-0201800P Claim 4; Page; 77pp; English Sellman BR; (HARD) HARVARD COLLEGE WPI; 2002-017725/02 anthracis. Sequence 735 AA; WO200182788-A2 Collier RJ, 08-NOV-2001 Synthetic Bacillus

ö 240 120 120 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 240 300 GRIDKNVSPEARHDLVAAYPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTSRTHT 300 420 420 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 9 DGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT NANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADENOLSOILAPNNYYPSKNLAPIA 1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPWVYTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADTARL 1 EVKQENRILINESESSSQGILGYYFSDINFQAPMVVTSSTTGDISIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY ; 0 Length 735; Indels 99.7%; Score 3759; DB 5; llarity 99.7%; Pred. No. 6.4e-248; Conservative 0; Mismatches 2; Query Match Best Local Similarity Matches 733; Conserv 181 61 61 121 121 181 241 241 301 301 д ઠે qq 유 ð g δ 셤 ઠ 8 g à ò

The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1484-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483) 009 900 99 720 720 480 Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein. 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNAINIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis. LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR /note= "Wild-type Phe substituted by Ala" Key Location/Qualifiers Misc-difference 427 Š IKKILIFSKKGYEIG 735 ikkilifskkgymig 735 421 481 481 541 601 601 661 661 721 721 g D. g g 8 8 8 δ ò 8 ઠે

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us-09-848-909a-13.rag

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in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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Best Local Simi
Matches 733;
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moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                               LNAQKDASSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
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Synthetic.
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Length
Score 3760; DB 5;
Pred. No. 5.4e-248;
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nthrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.

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substituted substituted

/note= "Wild-type Lys /note= "Wild-type Asp

Misc-difference 425

WO200182788-A2

08-NOV-2001

Key Location/Qualifiers Misc-difference 397

anthracis.

Synthetic

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Pred. No. 8.2e-249;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Aam51498 Anthrax P				<u>ო</u>	Aae18288 Bacillus	Aay56961 B. anthra					Aam50707 Bacillus	Aae07903 C. botuli	01 C.	Aae07900 C. botuli	Aae07902 C. botuli	Aae35719 Clostridi	Aaw60224 Bacillus	Aay59277 MIS toxin	Aar91239 B. cereus
AAM51498	AAM51497	AAM51496	AAM52113	AAR60193	AAE18288	AAY56961	AAE18285	AAE18287	AAE18286	AAE18284	AAM50707	AAE07903	AAE07901	AAE07900	AAE07902	AAE35719	AAW60224	AAY59277	AAR91239
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3626	3620	3613	3607	3576	3037	2898	2488	2173	1624	1338	1275	839.5	838	834	825.5	810	767.5	767	166
26	27	28	29	30	31	32	33	34	35		37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

Anthrax, PA, protective antigen; antibacterial; pore-forming toxin; B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein. The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1484-AAMS1850), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the moiety is anthrax protective antigen (PA) and using these mutants or Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis. /note= "Wild-type Asp substituted by Lys" Misc-difference 427 Ala" /note= "Wild-type Lys substituted by Asp" /note= "Wild-type Phe substituted by Location/Qualifiers Misc-difference 397 Anthrax PA mutant K397D/D425K/F427A. AAM51495 standard; protein; 735 AA. Claim 4; Page; 77pp; English. 04-MAY-2001; 2001WO-US014372. 04-MAY-2000; 2000US-0201800P 01-FEB-2002 (first entry) Collier RJ, Sellman BR; (HARD) HARVARD COLLEGE WPI; 2002-017725/02: Misc-difference 425 Bacillus anthracis.

1395 NKNHNFINSYPDLNENEKKKKINIF 1419

Search completed: May 3, 2004, 19:40:03 Job time : 38.6261 secs

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2179 41; 1982 IDDIKNNETYPYIKIDKKEKNNEDK---KNKYMYNKNDNKNIMKGSSN----KSMKKNNKNS 2036 1862 KHNNYTFNKEENNLKSIFKYNNNNINEKDDIPKSIQSSFINEDNIAYYNKEGNNMKLKN 1921 2037 NKMKH-------IPLSVNNKGY-----NKSSINKKYENNIN------KNNK 2069 2180 TI------YTWVNNIDTNYMYNKYFDSKKANINHVPLLNNVPYLN------NDL 2221 2222 LINNVILNQNNMNNLENLNTNTIGSVQPFVTCPDFY--ANNIKSIYLD------PNLQ 2271 58 Q-YFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDD-----QEVINKASNSNK---- 105 -IRLEKGRLY-QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS 163 164 RKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSP 223 224 EXWSTASDPYSDF--EKVTGRI-DKNVSPEARHPLVAAYPIVHVDME------NIILS 272 273 KNEDOSTONTDSETRIISKNISISRIHISEV-HGNAEVHASFFDIGGSVSAG-FSNSNSS 330 331 TVAIDHSLSLAGERTWAETMGLNTA-----DTARLNA-----NIRYVNTGTAPIYNVL 378 379 PITSLVLGKNQTLATIDADENQLSQ----ILAPNNYYPSKNLAPIALNAQKKFSSTPITM 434 3 KQENRLLNESESSSQGLLGY-YFSDLNFQ--APMVVTSSTTGDLSIP--SSELENIPSEN 57 DECURNATION N.A.

MEDLINE-22255705; PubMed=12368864;

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MEDLINE-22255705; PubMed=12. Manage I.T., James K.W., Eisen J.A., Kutherford K., Salzberg S.L., Craig A., Kyee S., Chan M.-S., Nene V., Shallom S.J., Sub B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengul S.J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Wengall C., Camucings L.M., Subramanian G.M., Mungall C., Davis R.W., Fraser C.M., Barrell B.;

"Genome sequence of the human malaria parasite Plasmodium 2125 KANDUNINDINININFERINDININSYNVLNINKVPYDNINI-----DEGNYINYGPIYAPDGS Query Match
5.3%; Score 201.5; DB 5; Length 2849;
Best Local Similarity 20.6%; Pred. No. 0.67;
Matches 170; Conservative 134; Mismatches 333; Indels 189; Gaps Přil 0392. Plasmodium falciparum (isolate 3D7). Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TaxID=36329; Nature 419:498-511(2002). EMBL, AB014841; AAN35975.1; -. Hypoth Attical Protein. SEQUENCE 2849 AA; 335916 MW; BS515D173D96B813 CRC64; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 101-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein. 717 682 NDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS PRT; 2849 AA PRELIMINARY; [1] SEQUENCE FROM N.A. falciparum. 106 RESULT 13 Q8IHY4 a B ò ò 원 g ઠે 셤 જે g ઠે 요 δ ઠ ò 8

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MEDLINE=22061436; PubMed=12004073;
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MEDLINE=22061456; PubMed=12004073;
MICHARAPINE B., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
"Comparative Genome Sequencing for Discovery of Novel Polymorphisms is archaracis.";
Science 296:2028-2033(202).
GO; GO:0046821; C:extrachromosomal DNA; IEA.
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hes 68; Conservative 38; Mismatches 54; Indels 23.
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Protective antigen-related protein, (pX01-111).
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                                                                                                                                                                                   344 --TGE-SFSQGLSINTGESAYINPNIRYYNTGTAPVYNVTPTTTIVIDK-OSVATIKGQE 399
                                                                                                                                                                                                                                                              SLIGDYLNPGGTYPIIGEPPWALNTMDQFSSRLIPINYNQLKSIDNGGTVMLSTSQFTGN 459
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                                                                                     ----SVSAGFSNSNSSTVAIDHSL 338
                                                                                                                                                                                                                                      NQLSQILAPNNYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGN 458
          WSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE 285
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Shure From J., Pang Y.;
"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";
"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";
"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";

GO, GO: 0005576; C: extracellular; IEA.
GO, GO: 0010570; F: textin activity; IEA.
GO, GO: 0005405; Pathogenesis; IEA.
InterPro; IPR003896; Anthrax toxinB.
Pfam; PR03495; BlankYroxB; I.
PRINTS; PR03391; BINARYTOXB; I.
SEQUENCE 775 AA; 87110 MW; 416B25394361B731 CRC64;
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                              SLAGERTWAETWGLNTADTARLWANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIDADE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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Last annotation update)
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SEQUENCE I
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SEQUENCE FROM N.A.
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NCBI_TaxID=1491;
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Best Local Simi
Matches 223;
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--PFIPNNNFFDVRFFSAAWEDEDLDTDNDNIPDAYEKNGYII----KDSIAVKWNDSFA 249
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            SEQUENCE FROM N.A.
STRAIN=NCIB 10748;
MEDIJINE=NCIB 10748;
Perelle S., Gibert M., Boquet P., Popoff M.R.;
"Characterization of Clostridium perfringens iota toxin genes expression in Escherichia coll: ";
infect. Immun. 61:5147-5156 (1993).
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212 875 IOTA TOXIN COMPONENT IB.
875 AA; 98468 MW; C9AE092CD3818921 CRC64;
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=NCIB 10748;
POPOÉTÉ M.R.;
Submitted (4045-1995) to the EMBL/GenBank/DDBJ dat
EMBL; X73562; CAA51960.1; -.
PIR; 140862; 140862.
HSSP; P13423; 140862.
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HSSP; P13423; P244109Geneeis; 1EA.
GO; GO:0009405; P; Pathogeneeis; 1EA.
InterPro; IPRO3996; Anthrax toxinB.
PFan; PF03495; Binary toxaB.
PFNIYS; PR01391; BINARYTOXINB.
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IIKEQLKYLDDKKIYNV----KLERGMNILIKVPSYFTNFDEYNNFP--ASWSNIDTKNQ
                                                                                                     -----IVEIEDTEGLKEVIND
                                                                                                                                                                         : : | : | : : | : : | : : DGLQSVANKLSGETKIIIPMSKLKPYKRYVFSGYSKDPSTSNSITVNIKSKEQKTDYLVP
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 24, Last annotation update)
C2 toxin (ComponentII).
C1ostridium botulinum.
Bacteria; Firmicutes; Clostridia, Clostridiales; Clostridiaceae;
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larity 35.3%; Pred. No. 2.3e-30;
Conservative 118; Mismatches 227; Indels
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STRAIN=type C;
MEDLINE=99323874; PubMed=9659689;
Kimura K., Kubota T., Ohishi I., Isogai H., Isogai E
Wim gene for component-II of botulinum C2 toxin.";
Vet. Microbiol. 62:27-34(1998).
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488
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                                                                                                                                                                                                TTKPDMTLKEALKIAFGFNEPNGNLQYQCKDITE--FDFNFDQQTSQNIKNQLAELNATN 573
                                                                                                                                                                                                                                                                                     IYNV----QLERGMKILIKTSTYFNNFDGYNNFPSSWSNVDSNNQDGLQNAANKLSGETK 658
                                                                                                                                                                                                                                                                                                                                            659 IVIPMSKLNPYKRYVFSGYLKNSSTSNPITVNIKAKEQKTYNLVSENDYKKFSYBFETIG 718
                                                                                                                                                                                                                                                                                                                                                                         .....IAVGADESVVKEAHREV----I 620
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----DQGKTVSRNTTNSKTDANTAGVAINIAYQNGF---TGSITTNYSHTTENSTAVQNS 373
                                                                                                                                                                                                                                                                                                                                                                                                                                  NSSTEGLLLN-----IDKDIRKILSGYIVEIE-DTEGLKEVINDRYDMLNISSLRQD
                                                                                                 ---NGE-SWNTSLSINKGESAYINANVRYYNTGTAPMYKVTPTTNLVL-DGDTLTTIKAQ
                                                                                                                                                                                                                                                                                                                                                                                                     RDASNIEITLISSGTIFLDNLSITELNSTPEILKEPDIKVPSDQEII-DAHKKYYADLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FACTOR 20309;
Chang S.Y., Song K.P.;
"ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain CUGG 20309;
"ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain CUGG 20309."
Submitted (WAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP271719; AAF81761.1; -.
EMBL; AP271719; AAF81761.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; F:toxin activity; IEA.
GO; GO:0005976; P:toxin activity; IEA.
GO; GO:0005876; P:toxin activity; IEA.
InterPro; IPR003896; Anthrax toxinB.
--- npn,448: Binary toxB; 1.
                                                                                 ENQLSQILAPNNYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYG
                                                                                                                                          NIATYNFENGRVRVDT-GSNWSEVLPQIQETTARIIFN-GKDLNLVERRIAAVNPSDPLE
                                                                                                                                                                                                                                                         IYTVLDKIKLNAKMNILIRD-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium difficile.
Bacterin Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium:
NCBI_TaxID=1496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838 PKINYVNFRSY-----FISGENVMPXKKLRIYALIPEN----
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Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
CdtB.
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                                                                                                                                                                                                                                                                                                                                                AIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           283 DSETRIISKNISTSRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSSIVAIDHS----
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                                                                                                                                                                     QENRILLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN-IPSENQYFQS
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01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.ONV-1996 (TrEMBLrel. 24, Last annotation update)
10.4 LOXIN component Ib precursor.
10.4 toxin component Ib precursor.
10.5 training perfringens.
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         Length 876;
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23.2%; Score 875.5; DB 2; Similarity 31.4%; Pred. No. 3.4e-33; 0; Conservative 140; Mismatches 280;
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    Query Match
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Matches 250;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 FDPKLMSDWEDEDLDIDNDNIPDSYBRNGYII----KDLIAVKWEDSFAE-QGYKKYVSN 260
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                                                                                                                                                  Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae, Clostridium.
                                                                                                                                                                                                                                                                                                                         Preclic 5. Glbert M., Bourlloux P., Corthier G., Popoff M.R., "Production of a complete binary toxin (actin-specific ADP-ribosyltransferase) by Clostridium difficile CD196."; Infect. Immun. 65:1402-1407(1997).

EMBL: 176081; AABS7305.1; -...

HSSP; P13423; 1ACC.

GO, GO:000576; C:extracellular; IEA.

GO, GO:001670; F:toxin activity; IEA.

GO, GO:001670; F:transferase activity; IEA.

GO, GO:001670; F:transferase activity; IEA.

GO, GO:001670; F:transferase activity; IEA.

GO, GO:001670; F:transferase activity; IEA.

GO, GO:001670; F:transferase activity; IEA.

HREPPICO: IPROGRAMS (AMPLIAN LOXINE).

FILE TOXING (AMPLIAN LOXINE).
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                            MEDLINE=97230316; PubMed=9119480;
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24,
                    01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                             ADP-ribosyltransferase.
                                                                                                                                          Clostridium difficile.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                          NCBI_TaxID=1496;
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                                                                                                                                 653 ETKIKIPMSELKPYKRYVFSGYSKDPLTSNSIIVKIKAKEEKTDYLVPEQGYTKFSYEFE
                                                                                                                                                                                  657 NDRYDMENIS-SERQDGKTFIDFKKYND--KLPLYISNPNYKV-----NVYAVTKENT
                           599 KIYNV----KLBRGMNILIKTPTYFTNFDDYNNYP--STWSNVNTTNQDGLQGSANKLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 AIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR
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573 NIYTVLDKIKLNAKMNILIRDKRFHY---DRNNIAVGADESVVKEAHREVINSSTEGL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQ-YFQS
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                                                                                      -----LLNIDKDIRKILSGY-----IVEI----EDTEGL----
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A Glbert M., Perelle S., Daube G., Popoff M.R.;
Clostridium spiroforme toxin genes are related to C. per.
Clostridium spiroforme toxin genes are related to C. per.
Cyste. Appl. Microbiol. 20:337-347(1997).
SYST. Appl. Microbiol. 20:337-347(1997).
KNBL; X97969; CAA66612.1;
RSSP; P13423; 1ACC.
A GO; GO:0005576; C:extracellular; IEA.
A GO; GO:0015070; F:toxin activity; IEA.
A GO; GO:0015070; F:toxin activity; IEA.
A GO; GO:0015070; F:toxin activity; IEA.
A GO; GO:0015070; B:nary toxis; IEA.
B Fem.; PR03495; B:nary toxis;
B PRINTS; PR01391; BINARYTOXINB.
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Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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Bacteria, Firmicutes; N
NCBI_TaxID=29348;
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DMLNISSLRQDGKTFIDFKKYNDKLFLYISNPNYKVNVYAVTKENTIINPSENGDISTNG
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          GO; GO:0005576; C:extracellular; IEA.
GO; GO:0046821; C:extrachromosomal DNA; IEP.
GO; GO:0019070; F:toxin activity; IEA.
GO; GO:0019070; F:toxin activity; IEA.
InterPro; IPR003896; Anthrax toxinB.
Print; PR03495; Binary toxB; I.
PRINTS; PR01391; BINARYTOXINB.
                                                                                                                                                                                                                                                  97.4%; Score 3676; Lilarity 99.2%; Pred. No. 1e-1
Conservative 1; Mismatches
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743
743 AA;
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Best Local Similarity
Matches 716; Conser
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Fasanella A., Francia M., Ciuchini F.;
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Factors can any year of the genes encoding for the major virulence
Factors of bacillus Anthracis vaccine strain 'Carbosap'.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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TOTOTION SPECKER: 34, Last annotation update)

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RA WOOV, G. Walliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

RA Gouros J., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RODIES S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Gentles S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA Holroyd S., Hornsby T., Howarth S., Muchle E.J., Hunt S., Jagels K.,

Money P., Moule S., Mungall K., Murphy L., Niblet D., Odell C.,

RA Money P., Moule S., Pearson D., Quall M.A., Rabbinowitsch E.,

RA Skelton J., Siamonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Siamonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Volraert G., Aert R., Robben J., Grymonprez B.,

RA Moultjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Purnelle B.,

RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Bucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

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4.2%; Score 158; DB 1; Length 1957;
Best Local Similarity 20.3%; Pred. No. 2.7;
Matches 176; Conservative 134; Mismatches 327; Indels 232; Gaps
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerntiti L., Lowe T., McComble W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; "The genome sequence of Schizosaccharomyces pombe.";
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EMBL, AB027811; BAA97115.1; -.
EMBL, AB027811; BAA97115.1; -.
EMBL, AB027811; BAA97115.1; -.
EMBL, AB027811360; -.
Sporulation; Coiled coil.
DOMAIN 198 1235 COILED COIL (POTENTIAL).
DOMAIN 1320 1471 COILED COIL (POTENTIAL).
DOMAIN 1481 1732 COILED COIL (POTENTIAL).
SEQUENCE 1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBUNIT: Monomer.
-1- SUBCELLULAR LCCATION: Spindle pole body.
-1- SIMILARITY: Belongs to the MPC70 family.
                                                                                                                      Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -QPIESNIKMTLEDNNVTSNPSEFTPNMVNSEISNLPKDKS------GIPEFTPAD
                                                                                           323 GVLSSNIAGTNPLSSDGAYT-----BQFQHYKN-NSISSQPASYHSVQETNKISPKDFS
                                                                                                                                                                            DEDLFGDSNKSNSTVESNKSISDEI-----TEDMFEMSDEEENNNN----
                                                                                                                                                                                                                                                                                                  SGT-----TKRLNGKRKYLD---IPIDEMTLPTSPLYMDPGAPL-PVETPRDRRKSVF
                                                                                                                                                                                                                                                                                                                                                                              LVERR-----IAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : | : | : | : | ITSNKEGFNSIWKIPQNDIPQTESPLKTVDSSI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                615 AHREVINSSTEGLLL------EIEDT
                                                                               27 INFOAPWV-VISSITGDLSIPSSELENIPSENOYFOSAI--WSGFIKVKKSDEY----
                                                                                                                     -----TPATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQI----KIQYQREN
                                                                                                                                                             PTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIP
                                                                                                                                                                                                     DSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKW-STASDPYSDFE-----
                                                                                                                                                                                                                   TELEANGRSLEKVNNSVSKTGSVDTLHNKEGTLEQREQNENLPSDKSDSMVDKELFGEDE
                                                                                                                                                                                                                                             ------KVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSET
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                                          Length 1420;
                                                            Indels
887 887 T -> P (IN REF. 2).
1284 1284 Y -> S (IN REF. 2).
1420 AA; 160000 MW; 7F6CF4BBE0FAC918 CRC64;
                                       4.2%; Score 159; DB 1; Le
llarity 19.1%; Pred. No. 1.6;
Conservative 129; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIINPSENGD-----TSTNGIK--KILIFS 728
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                                       Query Match
Best Local Similarity
Matches 155; Conserv
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  CONFLICT
CONFLICT
SEQUENCE
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CAG pathogenicity island protein 26).

GN CARO OR CAI OR CAG26 OR JHP0495.

CRAPA OR CAI OR CAG26 OR JHP0495.

CRAPA OR CAI OR CAG26 OR JHP0495.

CRAPA OR CAI OR CAG26 OR JHP0495.

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CRAPA OR CAG26 OR JHP0495.

CRAPA OR CAG26 OR JHP04921682;

RA DIM R.A., Ling L. S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., RA Alm R.A., Moonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Milis D.M., Ives C., A Thust T.J., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., RA Gibbon R. J., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F., R. "Genomic sequence comparison of two unrelated isolates of the human R gastric pathogen Helicobacter pylori.";

CA THURLES JR. CACA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA OR CAGA 
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PIR; B71924; B71924.
InterPro; IPR005169; CagA.
InterPro; IPR004355; IVSec_cagA.
Pfam; PP03507; CagA; I.
PRINTS; PR01553; TYPE4SSCAGA.
Antigen; Complete proteome.
DOMAIN 246 249 POLY-THR.
DOMAIN 246 249 POLY-THR.
SEQUENCE 1167 AA; 129729 MW; FD5E866B81CEBD0F2 CRC64;
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19.6%; Pred. No. 1.3;
ative 145; Mismatches 313;
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Best Local Similarity 19.6%; Prev
Matches 157; Conservative 145;
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CAGA HELPJ STANDARD; PRT; 1167 AA.
09ZLT1;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
CYCOTCZ1001 (Rel. 40, Last annotation update)
CYCOTCZ1001 (Rel. 40)

RESULT 14
CAGA_HELPJ
ID _CAGA_HI
AC _Q9ZLT1
DT _16-OCTDT _16-OCTDT _16-OCTDE _CYTOLO3

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----VRYKDIGIHYDRDCNKDKKVIAITDASVGSEYDAQSRIGVILMYGMNIFNVYSNKS 1676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 OREN----PTEKGLDFKLYWTDSONKKEVISSDNLOLPELKOKSSNSRKKRSTSAGPTVP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 274 NEDOSTQNTDSETRIISKN--TSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSST 331
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                                                                                                                                                                                                                                                                                                                                                     Query Match
4.2%; Score 160; DB 1; Length 1803;
Best Local Similarity 19.4%; Pred. No. 1.9;
Matches 161; Conservative 121; Mismatches 278; Indels 268; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1129 -----SINDY----KF
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reveals 19 open reading frames including URA2 (5' end), TRK1, PBS2, SPT10, GCD14, RBE1, PHO86, NCA3, ASP1, CCT7, G2F3, two tRNA genes, three remnant delta elements and a Ty4 transposon."; Yeast 12:1471-1474(196)
                                                                                                                                                                                                          EMBL; Z49389; CAA89409.1; -.
SGD; S0003649; YUL113W.
InterPro; IPR001584; Rve.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00665; rve; 1.
SMART; SM00343; ZnF_C2HC; 1.
Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                     1677 INRCVSSTEABLHAIYEGYADSBTLKVTLKBLGEGDNNDIVMITDSKPAIQGLNRSYQQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E., Berno A., Carpenter J., Cherry J.M., Chung E., Duncan M., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Kinant A., Yelton M., Botstein D., Davis R.W.;
Submitted (AuG-1995) to the EMBL/GenBank/DDBJ databases.

-!- FINGTION: Component of the RNA polymerase II holoenzyme and the mediator of activation subcomplex.

-!- SUBCELLULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                         [1] — SEQUECE FROM N.A.
SEQUECE FROM N.A.
SEQUECE FROM N.A.
MEDLINE=52286.;
MEDLINE=52293223; PubMed=7774808;
MEDGARTHOR C.J., Thompson C.M., Zhang J., Chao D.M., Liao S.-M.,
Koleska A.J., Okamura S., Young R.A.;
"Association of an activator with an RNA polymerase II holoenzyme.";
Genes Dev. 9:897-910(1995).
                                                                                                                                                                SRB9 YEAST STANDARD; PRT; 1420 AA.
P18911.
01-PEB-1996 (Rel. 31, Created)
01-PEB-1996 (Rel. 33, Last sequence update)
01-CT-1996 (Rel. 34, Last annotation update)
Suppressor of RNA polymerase B SRB9 (SCA1 protein).
SRB9 OR SCA1 OR SSN2 OR YDR443C.
SACCharomyees cerevisiae (Baker's yeast).
Bukaryota; Pungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales;
                                                                            ---DFKKY
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SEQUENCE FROM N.A.
Yuryev A., Corden J.L.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
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POLY-GLU.
POLY-SER.
POLY-LEU.
POLY-GIN.
D -> E (IN REF. 2).
T -> S (IN REF. 2).
VK -> GE (IN REF. 2).
                                                           ----EVINDRYDMLNISSLRQDGKTFI----
TEGLLLNIDKDIRKILSGY----
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EMBL; U09176; AAA18614.1; --
EMBL; U33007; AAB64875.1; --
PIR, B57062; B57062.
GermOnline; 140935; --
TRANSRC; TO2183; --
SGD; S0002851; SSN2.
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951:TIINSIEQNSGWKLCIRNG----NIEWILQDVN-----RKYKSLIFDYSESLSHTGYTNK 1001
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                   -GRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEV 145
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                                                                                                                  ----DSTCIKVKNNRL---
                                                                                   146 ISSDNLQL-PELKQKSSNSRXKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLS
                                                                                                                                                   PWISN-----IHEKKGLTKYKSSPEKWSTASDPYS-DFEKVTGRIDKNVSPEARHPLV
                                                  SQYNVKNRTHYFSRHYLPVFANILDDNIYTİRDGF----hLİNKGFNIE-----
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Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                         110 NSGONIERNPALOKLSSESVVDLFTKVCLRLTKNSRD-
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RA ROQUES B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;

"Cleavage of members of the synaptobrevin, VAMP family by types D and
F Potulinal neurocroxins and tetanus toxin.";

"Biol. Chem. 269:12764-12772 (1994).

"FELDALL Chem. 269:12764-12772 (1994).

"FELDALL CHEMPERSE. IT BINDS TO PERIPHERAL STUAPESE, IS INTERNALIZED AND MOVES BY RETROCRADE TRANSPORT UP THE AXON INFO THE SPINAL CORD WHERE IT CAN MOVE BETWEEN POSTSYMAPTIC AND PRESYMAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC ENDOPERTIDASE THAT CLEAVES THE 60-Lys-[-LEU-61 BOND OF SYMAPTOREVINS.] AND

"C ATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

"C -I- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

"SYNAPTORE BLINGs 1 zinc ion per subunit (By similarity).

"SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel of formation and toxin binding, respectively.

"SUBCLIANEOUS: Horder are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.

"MISCELLANEOUS: BOTULINUM TYPES D NEUROTOXIN IS SYNTHESIZED BY D STRAIN OF CLOSTRIDUM SOUTHINUM WHICH CARRY THE APPROPRIATE

BACTERIOPHAGE.

"I SIMPLATIY: Belings to peptides family M27.
                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstanton the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.3%; Score 162; DB 1; Length 1276;
ilarity 20.7%; Pred. No. 0.96;
Conservative 122; Mismatches 291; Indels 214; Gaps
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Saccharomycetes;
                                                                                                       SEQUENCE.FROM N.A.
STRAIN=S288C / FY1679;
MEDLINE=97103775; PubMed=8948101;
Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;
"Sequencing analysis of a 40.2 kb fragment of yeast chromosome
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103

SIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNS :|||| : || ::| | ::| TIPSSWISNI---DKY--KKIFSEKYNFDKDNTGNFVVNIDKFNSLYSDLTNVMSEVVYS

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308 EVHASFFDIGGSVSAGFSNSNSSTVAID----HSLSLAGERTWAETMGLNTADTARLNAN 363
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A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volckaett G., Aert R., Robben J., Grymonprez B., Meltjens I., Vangtreels E., Rieger M., Schaefer M., Meller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., A Goffeau A., Cadleu E., Dreano S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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4.3%; Score 163; DB 1; Length 1385;
Best Local Similarity 19.1%; Pred. No. 0.96;
Matches 146; Conservative 129; Mismatches 292; Indels 198; Gaps
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MEDLINE-20143585; PubMed=10679021;
Min Amberg D.C.;
The secretory pathway mediates localization of the cell polarity
acquiacr Aighy-Naudep.";
Mol. Biol. Cell 11:647-64[2000).
-:- FUNCTION: Involved in the organization and/or function of the
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DOMAIN 1009 1096 COILED COIL (POTENTIAL).

SEQUENCE 1385 AA; 154325 MW; ABB3D40CC4FF7537 CRC64;
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-!- SIMILARITY: TO YEAST BUD6.
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814 ELGELFSNVYKISFSGDSYELNIED-----PDTKISYLLEDLSDLKYKSLVSFMFKEQ 866
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670 NTGA-----SAKLINDPSSTITVSDVYPKKPASPVEITEPPSSALVSATSPTTNVP
                                                                                                                                                                                                                                            420 ALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSE
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STRAIN=D-SA, and D-1873;
MEDLINE=89339741; PubMed=2668193;
Moritabi K., Syuto B., Kubo S., Oguma K.;
"Molecular diversity of neurotoxins from Clostridium botulinum type
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IDENTIFICATION OF SUBSTRATE.
MEDLINE=94230352; PubMed=8175689;
Yamagaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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SEQUENCE FROM N.A.
STRUMBUD/-3;
MEDLINE=BUD/-3;
MEDLINE=91016853; PubMed=2216736;
Binz T., Kurazono H., Popoff M.R., Eklund M.W., Sakaguchi G.,
Kozaki S., Kriegistein K., Henschen A., Gill D.M., Niemann H.;
Nucleotide sequence of the gene encoding Clostridium botulinum
neurocoxin type D.",
Nucleic Acids Res. 18:5556-5556(1990).
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P19321;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-203 (Rel. 41, Last annocation update)
Botulinum neurocoxin type D precursor (EC 3.4.24.69) (BoNT/D)
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SEQUENCE FROM N.A.
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1079 LKKVTDTDGTVTSYDYDSEGRLVKQYSANSTEAKPVFTEYQYSGHRLEKAINAKKETYVY 1138
                                                                                                                                                                GKGFETLDLGNOTSWTTKGKKIWPTSAEIKAGKYALHLKDGSGAELPINPGPTYKWAGGD 718
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                          DPSPVYNNANGNYKGKKOVYSFTLVAYDANGETIPTAPFNPTFHEGAEFLGTEEVWSIIDI
                                                                      --DOSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAG------FS
                                                                                                IFDQGEGAMSAPAKPVIPNVGKAQAPSAKGYNNGNA-TGYFDLSWKAVSGATGYKVQVFN
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Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgontos V., Gwilliam R., Hayles J., Baxer S., Basham D., Bowman S., Contors K., Brown D., Erown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamiln M., Harris D., Hidalgo J., Hodgson G., Holrods S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mconey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares S., Stevens K.,
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013735, Q9UTJO;
15-UL1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Actin interacting protein 3 homolog.
FAT1 OR SPAC15A10.16 OR SPAC15E1.01.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetales; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetales; Schizosaccharomycetales; NCBI_TAXID=4896;
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                                                                                                                                       NSNSSTVAIDH--SLSLAGERTWAETMGLNTADTA-
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Subtilist; BG10797; wapA.

R InterPro; IPR00530; CBM_CenC.

AR InterPro; IPR00530; CBM_CenC.

DR Pfam; PF05593; RHS_repeat; 11.

DR Pfam; PF05593; RHS_repeat; 2x; 17.

DR TIGRPAMs; TIGRO143; YD_repeat 2x; 17.

DR TIGRPAMs; TIGRO143; YD_repeat 2x; 17.

RW Cell wall; Repeat; Signal; Complete proteome.

FT SIGNAL

29 2334 WALL-ASSOCIATED PROTEIN.

FT SIGNAL

504 87 3 101 AA APPROXIMATE TANDEM REPEATS.

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31 X 21 AA APPROXIMATE TANDEM REPEATS
X(4) -G-X(4) -[YF]-X-D-X(2) -G-X(4).
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8.2%; Pred. No. 1.6;
ve 126; Mismatches 336;
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Foster S.J.; Molecular analysis of three major wall-associated proteins of molecular analysis of the product of Bacillus subtilis 168: evidence for processing of the product of gene encoding a 258 kDa precursor two-domain ligand-binding
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STRALH-168 / BOSC1A1;
MEDLINE-55219088; Pubmed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
                                                                     Wall-associated protein precursor.
WAPA OR NITG OR BSU39230.
Bacillus subtilis.
Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                          Last sequence update)
Last annotation update)
 2334 AA.
                                                                                                                                                                          STRAIN=168;
MEDLINE=93302506; PubMed=8316082;
                                                                                                                                                                                                                                                                                Microbiol. 8:299-310(1993)
                         01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last seq
10-0CT-2003 (Rel. 42, Last anno
STANDARD;
                                                                                                                                                           SEQUENCE FROM N.A.
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EMBL; L05634; AAA22883.1; -. EMBL; D31856; BAA06656.1; -.

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; D29985; BAA06260.1; -. ; D83026; BAA11683.1; -. ; Z99124; CAB15959.1; -. S32920; S32920.

EMBL; EMBL; EMBL; PIR; S

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                                                                                                                                                                                                                                                                                                                                                                                                                                     RA KUDINE-SPOR4613; PubMac=9384377;
RA KURSINE-SPOR4613; PubMac=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Barstser L., Brans A., Braun M., Briggell S.C., Bron S., Bruschi C., Brans A., Braun M., Briggell S.C., Bron S., Raberilet S., Bruschi C., Brans A., Braun M., Briggell S.C., Bron S., Raberilet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A., R.A. Chois.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Beritz C., Fujita M., Pujita Y., Puma S., Galizzi A., Galleron N., A. Eritz C., Fujita M., Pujita Y., Puma S., Galizzi A., Galleron N., A. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., A. Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Cones L., A. Coris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., R., A. Koetter P., Koningstein G., Krogh S., Kumano M., Klein C., Rotita R., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Rotine A., Liu H., Masuda S., Mauel C., Medigue C., Resecan E., Puli P., Mizuno M., Moestl D., Nakai S., Noback M., R. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Bractoni C., Roche E., Roche B., Roch B., Rey M., Sadaie Y., Raeuchi M., Tamakoshi A., Serior S., Schroeter R., Stoffone F., Schleich S., Schroeter R., Stoffone F., Tarkegi T., Tarkapi T., Tarkapi H., Tarkamaru K., Tarkapi T., Tarkapi T., Tarkapi H., Tarkamaru K., Tarkapi A., Tarconi E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S., Weller S.,
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SUBCELLULAR LOCATION. MEMBRANE-ASSOCIATED. MAY BE RELEASED INTO THE MEDIUM.
INTO THE MEDIUM.
DOMAIN: HAS TWO LIGAND-BINDING DOMAINS, THE N-TERMINUS, HAS THREE 101 AA REPRATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED WOIT REPRATED AI TIMES.
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapA loci."; Microbiology 141:337-343(1995).
                                                                                                       SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
MEDLINE=97124196; PubMed=8969509;
YOShida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai I Miwa Y., Fujita Y.;
"Sequencing of a 65 kb region of the Bacillus subtilis genome containing the lic and cel loci, and creation of a 177 kb contisposering the apt-sacXx region.";
Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168
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   MOI. Cell 9:773-788 (2002).

-i- FUNCTION: Involved in chromosome cohesion during cell cycle and in DNA repair. Central component of cohesion complex. The cohesion complex is required for the cohesion of sister chromatids after DNA replication. The cohesin complex apparently forms a large proteinaceous ring within which sister chromatids can be trapped.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTIFICATION IN A COHESIN COMPLEX WITH SMC1; IRR1 AND MCD1, AND INTERACTION OF THE COHESIN COMPLEX WITH SCC2.

MEDLINE=99145468; PubMed=9990856;

MEDLINE=99145468; PubMed=9990856;

Toth A., Closk R., Uhlmann F., Galova M., Schleiffer A., Nasmyth K.;

"Yeast cohesin complex requires a conserved protein, Ecolo(Ctf7), to
establish cohesion between sister chromatids during DNA replication.";
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=W303;
MEDLINE=9747309; PubMed=9335333;
Michaelis C., Closk R., Nasmyth K.;
"Cohesins: chromosomal proteins that prevent premature separation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DENTIFICATION IN A COHESIN COMPLEX WITH SMC3; MCD1 AND IRR1, AND
                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Structural maintenance of chromosome 3 (DA-box protein SMC3).
SMC3 OR VIL074C OR J1049.
SACCHAROWCES CEREVISIAE (Baker's yeast).
Bukaryota; Fungi, Ascomycota; Saccharomycetiaes; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetaces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haering C.H., Loewe J., Hochwagen A., Nasmyth K.; "Molecular architecture of SMC proteins and the yeast cohesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sor F.J.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                            1230 AA
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                                                                                                                                               STANDARD;
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STRAIN=S288c / FY1678;
                                                                                                                                                                                                                                                                                                                                                                                                 sister chromatids.";
Cell 91:35-45(1997).
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chromatin, allowing sister composed of the SMC1 and SMC3 heterodimes trached via their hinge domain, MCD1/SCC1 which link them, and IRRI/SCC3, which interacts with MCD1. The cohesin complex also interacts with SCC2, which is required for its association with chromosomes.

-!- SUBCELULIAR LOCATION: Nuclear protein. Associates with chromatin. Before prophase it is scattered along chromosome arms. At anaphase, the MCD1 subunit of the cohesin complex is cleaved, leading to the dissociation of the complex from chromosomes, allowing chromosome separation.
-!- DOMAIN: The Iteration in thinge domain, which separates the large intramolecular coiled coil regions, allows the heterotypic interaction with the corresponding domain of SMC1, forming a V-shaped heterodimer. The two heads of the heterodimer are then connected by different ends of the cleavable MCD1 protein, forming a ring structure (By similarity).
-!- SIMIARITY: Belongs to the SMC family. SMC3 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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REMBL; X48881; CAA89466.1; -.
REMBL; X58880; S56850.
REMBL; CAA61313.1; -.
RILE; CAA61313.1; -.
RILE; CAA61313.1; -.
RILE; CAA61313.1; -.
REMBL; X56880; S56850.
REMBL; CAA61313.1; -.
REMBL; X56880; S56850.
REMBL; S56880; SMC3.
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the complex is cleaved and dissociates from
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1126 1161 ALA/ASP-RICH (DA-BOX).
1230 AA; 141336 MW; B152D88F7780341F CRC64;
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FLEXIBLE HINGE.
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19.8%; Pred. No. 0.34;
tve 136; Mismatches 355;
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NP BIND 32
DOMAIN 172
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Matches
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or send an email to license@isb-sib.ch)
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              858
                                                                   905
                                                                                                                                                                          995
                                                                                              634
                                                                                                                                                  694
STDKSTEDNTD----EXYFSAINYTN----VTGDSSCEDIIETASNVEE---NLRYCEKD
                                                                                                                                                                  | :: |: : | : ------
                                         547 ITEFDFNF-DQQTSQN---IKNQLA-----ELNATNIYTVLDKIXLNAKMYILIRDKR
                                                            ----SSTEGLLLNIDKD
                                                                                                                      --YKVRNSDLEDDESLKKELTKAEVVDKLDEEESEDSYEQDYADPEPGNDEGSNENIVKG
                                                                                                                                                635 IRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     new family of proteins, associate and function positively
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MEDLINE-96287652; bubMed=8686379;
MEDLINE-96287652; bubMed=8686379;
MEDLINE-96287652; bubMed=8686379;
Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
"Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI from Saccharomyces cerevisiae.";
Yeast 12:149-167(1996):
-!-FUNCTION: Associates with the SIT4 phosphatase in a cell cycle dependent manner. May be directly or indirectly involved in SIT4-dependent functions in budding and in normal G1 cyclin
                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96220458; PubMed=8649382;
Luke M.M., della Seta F., di Como C.J., Sugimoto H., Kobayashi Arndt K.T., a new family of proteins, associate and function posiwith the SIT4 phosphatase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95400292; PubMed=7670463; Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma Y.-1., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T., "Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Hyperphosphorylated in the absence of SIT4. SIMILARITY: Belongs to the SAPS family.
                                                                                              PHYDRNNIAVGADESVVKEAHR-EVIN-------
                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
SAPISS OR YFR040W.
                                                                                                                                                                                                                                                                                                  1000 AA
                                                                                                                                                                   the SIT4 phosphatase.";
Cell. Biol. 16:2744-2755(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 DINN-----LIDYQEQQQLD-------BSSQEDVYVESDTEQEEKEDDNNSNNKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 RRKRGSSSFGNDDINNNDDDDDANEDDESAYL----TKATIISEIFSLDIWLIS----ES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BVKQENRLLNESESSSQGLLGYYFS--DL----NFQAPMVVTSSTTGD----LSIPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 SELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDD-QEVINKASNSNKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 RLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R----STSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSP-----WISNIHEKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTKYKSSPEK-WSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 LVKNQSYLNKIWSIINQP------NFNSE-NSPLV--PIFLKINQNLLLTR-
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                                                                                                                                                                                   N -> T (IN REF. 2 AND 3).

TYSKSNYMIRDCFQNN -> DLFKIKLYDTRIVSKIM
REF. 2 AND 3).
DY -> EL (IN REF. 2 AND 3).

RYSSN -> POIQVI (IN REF. 2 AND 3).

My, AD4FBF0BC7CS88D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               262;
                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.5%; Score 171; DB 1; Length 1000;
Best Local Similarity 19.5%; Pred. No. 0.25;
Matches 173; Conservative 130; Mismatches 321; Indels 26:
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                                                Germonline, 140194; -. SGD; S001936; SAP155.
InterPro; IPR007587; SAP8.
Pfam; PF04499; SAPS; 1.
Phosphorylation; Cell cycle.
CONFLICT 663 663
EMBL; U50560; AAC49303.1;
EMBL; D50617; BAA09279.1;
                                                                                                                                                                                                                                                                                            818 82
1000 AA;
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SNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSN 162 :: : :	SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVK-NKRTFLSPWISNIHEKKG 215	LIKYKSSPEKWSTASDPYSDFEKVTGRIDKNUSPEARHPLVAAYPIVHV 264	DMENIILSKN-EDQSTQNTDSETRTISKNTSTSRTHT300 : :	SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTA 355	DTARLNVLG 386	KNQTLATIDADENQLSQILAPNNYYPSKNLAPIALN 422	AQKKESSTPITMNYNGFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVD 472	TGS	509 NPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGK 545 	DITEFDENFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRF 596	597 HYDRNNIAVGADESVVKEAHREVINSSTEGLLLINIDKDIRKILSGYIVEIEDTEG 651 ::	LKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYI- 689	NPNYKNNVYAVTKENT 706	
SNKIRLEKGRLYQIKIQYQRI :: : ; TSKYKLDKEEAQKKLIR	SRKKRSTSAGPTVPDRD :	LTKYKSSPEKWSTASDPYSDI : : FKTEVESS	DMENIILSKN-EDQSTQN :	SEVHGNAEVHASFFDIGG: 	DTARLNANI) LGAALNQIVMKTSEDVLQAI)		AQKKFSSTPITMNYNQFLEL : : : GGSKLERTSI-LNYDIKIK-	TGS		DITEFDFNFDQQT :: LTLEAASEQYSLDLDIEQAR	HYDRNNIAVGADESVVKEAH ::: YIEELTTAKSKIEEAISDLD		DEVEAALDESNVIRYDELKENT	
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RESULT 6
YM67 YEAST
AC 003661; 004988;
DT 0.1007-1997 (Rel. 35, Created)
DT 0.007-1997 (Rel. 35, Last sequence update)
DT 0.007-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 35, Last annotation update)
DT 10-OCT-2003 (Rel. 35, Last sequence update)
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STRAIN=S288c / AB972;
MEDLINE=97313268; PubMed=9169872;
Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome
NAIII.";
Nature 387:90-93(1997).
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4.6%; Score 173; DB 1; Length 1658;
Best Local Similarity 18.4%; Pred. No. 0.39;
Matches 157; Conservative 140; Mismatches 278; Indels 280;
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1658 AA; 187137 MW; 3893F968305A757D CRC64;
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0006348; P:chromatin silencing at telomere; IMP.
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PIR; S05603; S05603.

PDB; ICEG, 28-MAY-99.

ILTEPERO; IPRO009; EGF_like.

Pfam; PF00008; EGF; 1.

Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein; (POTENTIAL 1639 MENOZOITE GIRPACE PROTEIN 1.
11639 MENOZOITE GIRPACE PROTEIN 1.
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Query Match 5.0%; Score 190.5; DB 1; Length 1639; Best Local Similarity 20.6%; Pred. No. 0.051; Matches 171; Conservative 138; Mismatches 255; Indels 265; Gaps

966 SFINFVXSKADD-----INSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFD 1020 1077 T------KGLVKYYNGESSPLK 1103 1201 ESGSDTLEQSQPKKPASTHVGAES---NTITTSQ-NVDDEVDDVIIVPIFGESEEDYDDL 1256 -----QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS 168 64 IWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNS------NKIRLEKGRLY- 114 169 TSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLIKY---KSSP-- 223 224 ---EKWSTASDPYSDFE-----KVTGRIDKNVSPEAR------HPLVAAYPIVHVD 265 266 MENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS 325 382 -SLVLGKNQTLATIDADENQLSQILAPNNYYPSKNLAPIA---LNAQKKFSSTPITMNYN 437 -----QFLELEKTKQLRLDTDQV-YGNIAT-----YNFENGRVRVDTGSNWSEVL 481 534 NEPN----GNLOYQGKDITE------FDFNFDQQTSQNIKNQLAELNATNIYT 576 5 ENRL-LNESESSSOGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA 63 326 NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTT---PQIQETTARIIFNGKDLNLVERRIAAVNPSDPL-----ETTKPDM-TLKEALKIAFGF 115 438 셤 ઠે g ò g ठे 셤 ò 셤 δ 음 ò 유 ò ò ď ò g ð

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• -	S d	57 NQYPQSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASN 102

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                                          -----QFLELEKTYQLRLDTDQV-YGNIAT-----YNFENGRVRVDTGSNWSEVL 481
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       326 NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTT----
                                                                                                       -SLVLGKNOTLATIDADENQLSQILAPNNYYPSKNLAPIA---LNAQKKFSSTPITMNYN
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MEDLINE=86014355; PubMed=2995820;
MEDLINE=86014355; PubMed=2995820;
Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T., Freeman R.R.;
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01-FBB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
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Nature 317:270-273(1985).
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=5848;
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                                                                                                                                                                                                                  (Potential).
-!- PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4 kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont.
                                                                                                          REVISIONS, SEQUENCE FROM N.A.

BIJATA H.;

Submitted (JUM-1995) to the EMBL/GenBank/DDBJ databases.

-- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
"Polymorphism of the precursor for the major surface antigens of plasmodium falciparum merozoites: studies at the genetic level.";
EMBO J. 4:3823-3829(1985).
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Pfam; PF00008; EGF; 1.
Malaria, Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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SIGNAL 1 19
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Best Local Similarity
Matches 171; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
MEDLINE-89172073; PubMed=3148491; Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Leppla S.H. Schmidt J.J.; Schmidt J.J.; "Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis.";
                                                                                                                                                   MEDLINE=99445483; PubMed=10515943; MEDLINE=9944583; MEDLINE=99445483; PubMed=10515943; Medline=99445483; Medline=99445483; Medline=99445483; Medline=99445483; Medline=99448484; Medline=99448484, Medline=99448484, Medline=99448484, Medline=9949; Medline=994984, Medline=994984, Medline=994984, Medline=994984, Medline=994984, Medline=994984, Medline=9948484, Membrane-bound (Potential).
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EMBL, AAF064904; AAD32415.1; -.
PIR, G59104; G59104.
PIR, 139933; I39933.
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Hypothetical protein; PlearAnswam 162 182
CONFLICT 93 93
CONFLICT 184 204
                                                                            Bacillus anthracis.";
Gene 69:287-300(1988)
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                                                                                             EVKQENRILLNESESSSQG1LGYYPSDLNFQAPMVVTSSTTGDLS1PSSELEN1PSENQYF
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                                 Length 764;
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                               Score 3745; DB 1;
Pred. No. 2.7e-180;
1; Mismatches 4;
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                              Query Match
Best Local Similarity 99.3%;
Matches 730; Conservative
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; Transmembrane.

Plasmid;

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Plasmodium falciparum (isolate K1 / Thailand).
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCB_TaxID=5839;
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E: 1).
E1657B23AE4273FD CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozotic surface protein 1 precursor (Merozotic (PMMSA) (P190).
                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINES-68136024; PubMed=3004972; MEDLINES-68136024; PubMed=3004972; Mackay M., Goman M., Bone N., Hyde J.E., Scaife Stumenberg H., Bujard H.;
                                                      6.2%; Score 235.5; DB 134.6%; Pred. No. 1.7e-05;
                                                                                                     36; Mismatches
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            204 AA; 23029 MW;
                                                      Query Match
Best Local Similarity 34.6%;
Matches 56; Conservative
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MSP1_ELAFK
AC PO4932;
DT 13-AUG-1997
DT 01-FEB-1996
DT 01-CCT-1996
DT 01-CCT-1996
DT MSP-1.
OS PLASMOGLUM F
OC BUKARYOTA;
NO NCEL TAXID=5
RN SEQUENCE FRO
RP SEQUENCE FRO
RP SEQUENCE FRO
RR MACKAY M.;
SRAMACKAY M.;
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Bacillales; Bacillaceae; Bacillus.

Plasmid pXO1. Bacteria; Firmicutes;

[1] SEQUENCE FROM N.A. NCBI_TaxID=1392;

YPB1 BACAN

1D YPB1 BACAN

AC P13422; Q9X377;

DT 01-10-1990 (Rel. 40, Last sequence update)

DT 16-0CT-2001 (Rel. 40, Last sequence update)

DT 16-0CT-2001 (Rel. 40, Last annotation update)

BYPOTCHAIL Protein pX01-111.

GN PX01-111.

OS Bacillus anthracis.

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STRAIN=Weybridge;
MEDLINE=94131936; PubMed=8300513;
Koehler T.M., Dai Z., Kaufman-Yarbray M.;
Recaplation of the Bacillus anthracis protective antigen gene: CO2 and a trans-acting element activate transcription from one of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [14]
MUTAGENESIS OF GLN-512; ASP-541; LEU-543 AND ARG-621.
MUBDLINE=21125576; PubMed=11222612;
Mogridge J., Mourez M., Collier R.J.;
"Involvement of domain 3 in oligomerization by the protective antigen
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MUTAGENESIS OF PHE-581; PHE-583; ILE-591; LEU-595 AND ILE-603
STRAIN=Sterne;
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MUTAGENESIS OF DOMAIN 4 LOOPS
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REDIMEN B.R., Names 6., Collider R.J., Kimpel K.R., Lappla S.H., Liddington R.C.;

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 3, 2004, 19:27:02; Search time 8.2539 Seconds

(without alignments)

4636.784 Million cell updates/sec
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Title: US-09-848-909A-11
Perfect score: 3774
Sequence: 1 BVKQENKLINESESSQGLL.....TSTNOIKKILIFSKKGYEIG 735

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum D5 Seq length: 200000000 Post-processing: Minimum Match 100% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		23 bacillus an	22 bacillus an	32 plasmodium	33 plasmodium	08 mycoplasma											99 dictyosteli						87 caenorhabdi	e6 rattus norv	97 saccharomyc							78	31 clostridium	œ
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1 YNC7_YEAST	MYS3 SCHPO	1 TAO3 YEAST	1 PGCV HUMAN	1 BXE CLOBO	1 VACA HELPJ	1 HLYA PROMI	1 SWI6_YEAST	1 BXB CLOBO	1 YM41 YEAST	1 HMW1 MYCGE	1 GLN3_YEAST
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ž	PubMed=3148491;
Z	Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Leppla S.H.,
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RT	"Sequence and analysis of the DNA encoding protective antigen of
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RP	SEQUENCE FROM N.A.
S S	STRAIN=28, 33, BA1024, and BA1035;
ž	MEDLINE=99214082; Pubmed=10197996;
Ą	P.J., Keim P.;
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Ŗ	J. Bacteriol. 181:2358-2362(1999).
RN	[3]
ЯÞ	SEQUENCE FROM N.A.
22	STRAIN=V770-NP1-R / ATCC 14185;
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Z.	Kobiler D., Elhanany
A A	Gozes Y., Ba
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RT	"Attenuated nontoxinogenic and nonencapsulated recombinant Bacillus
RT	anthracis spore vaccines protect against anthrax.";
RT.	58 (2000)
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RP	SEOUENCE FROM N.A.
RC	STRAIN=Sterne;
X	MEDLINE=99445483; PubMed=10515943;
RA	Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
R.	Keim P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
RA FA	Martinez Y., Ricke D., Svensson R., Jackson P.J.;
RT	"Sequence and organization of pXO1, the large Bacillus anthracis
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RP	DOMAINS
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8 8	Singh Y. Klimpel K.K., Quinn C.P., Chaudhary V.K., Leppla S.H.;
¥ £	rective antigen is required
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Tue May

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hypthetical protein 2 - Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Species: Haemophilus ducreyi
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C;Accession: T31105
R;Mard, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
C;Accession: T31105
A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A;Accession: T31105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273 BQQGKVSIEGDSKPAKLANVTFAAGNLTYDVNTRDV-NRNTNPKKPITDNTRKDNIAISG 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 ESAGSMYGRNIKFIVTDKGAGVNHQGVIFAEDDINILTDDGNSRLNKVYADYVRVVGKDI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448 FRVINDTKIANDISKVS-----ARAADLQSGNINLDKASVLAHKLTLINISNDVSLNNQSK 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         375 YNVLPTTSLVLGKNQTLATIDADENQLSQI-----LAPNNYYPSKNLAPIALNAQKKF 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TDNVTLNSKSTLSAGELTFKKVKNVTLNNDSELAANN------LSLNA---- 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              428 SSTPITMNYNQFLELEKT--KQLRL---DTDQVYGNIATYNFENGRVRVDTGSNWSEVLP 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             637 -SHNVTLNNKSKLSAQKADIKAVNLTLNDTTE----LTAKNLDINSTTITNNGTIAGIFA 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 QIQETTARIIFNGKDLNLVERRI-AAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQ 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      692 NI--TTEKLNNKEKALILAEQNLNFTVNGSH--YENKGDIVSKDKATVTFSKNS---- 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 NNSIKEGNSQLVGLLGEN-KNLGSQAAKTIFNQVTGDQESKISGGLEVFGEKADLFIINP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205 PWISNIHEKKGLTKYKSSPEKWSTASDPYSD------FEKVTGRIDKNVSPEARHP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 LVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFF 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               315 DIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPI 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 TAGNMT---LNVTNNVTLNNDSELA-ANNLTLNVTKNVTLNDASKLSANKLDLNV---- 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DFTSNGSKLVNAQNQL-KVNVNNFTISQGDDITLIGNVTLNASGTFTNSGN 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YQGKDITEFDFNFDQQTSQNIKNQLAELNATNI-----YTVLDKIKLNAK-----
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4.7%; Score 178; DB 2; Length 4919;
Best Local Similarity 20.0%; Pred. No. 2.4;
Matches 182; Conservative 126; Mismatches 328; Indels 274;
  ----TNPNYSTLISELTSKRDSKNSITNSSNKSDIET 1087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119
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Search completed: May 3, 2004, 19:41:19 Job time : 16.0855 secs

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A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; A;Experimental source: strain IL1403 C;Genetics: A;Gene: yqfG
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Local Similarity 19.4%; Pred. No. 0.21;
les 160; Conservative 142; Mismatches 342;
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UC6009
Contrace-located membrane protein lmp3 precursor - Mycoplasma hominis
CiSpecies: Mycoplasma hominis
CiSpecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
CiAccession: JC6009
Riladefoged, S.A.; Jensen, L.T.; Brock, B.; Birkelund, S.; Christiansen, G.
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syste repeat homology gene J. Bacteriol. 178, 2775-2784, 1996
A,Title: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene A,Reference number: JC6009, MUID:96213016; PMID:8631664
A,Reference number: JC6009
A,Residuce: JC6009
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A,Residuce: L1302 <LAD>
A,Residuce: L1302 <LAD>
A,Gress-references: EMBL:X95601; NID:g1197335; FIDN:CAA64858.1; PID:g1197336
C,Genetics: A,Gene: Lmp3
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A,Gene 912 617 28; 500 560 958 997 266 635 824 GKNOTLATIDADENOLSOILAPNNYYPSKNLAPIALNAO----KKFSSTPITMNYNOFL 440 ENIILSKNEDOSTONTDSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSN 326 --QQAKTELEKEVQKANQAVASNN-TASMQSAKSSLDAKVTEITKKLE----TFNKDKDV : : : | | : : | | : : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : ELEKTKOLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGXDLNL KEKELEQTRKDIDEF-----KPKELEQTRKDIDEF------KPKELEQTRKDIDEF--------VERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQ NIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGAD---ESVVKEAHR 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF :: | : : | :: | :: | :: | :: | CUDEANKSIKEQLNALIDKÀNTLLPQLNDNDSEIVKAKESLNAEITNANKAVNQNDNASM 61 OSAIWSGFIKVKKSDEYTFATSADNHVTMMVDDQEVINKASNSNKIRLEKGR--LYQIKI QSA-------KSSLDDKVTKIQNQLTEFNKDXDAKFKELEQTRKDIDNFLT 119 QYQRENPTEKGL-----DFKLYWTDSQNKKEVISSDNLQLPELKOKSSNSR--KKRS TSAGPTVPDRDNDGIPDSLEVEGYTV----DVKNKRTFLSPWISNIHEKKGL-----DEANKSIKEQLSDSITNANQLLNKLVDSDKDIQKAKTELSQBIQSASQELNLNNPTSMQS -----TKYKSSPEKWSTASD-PYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDM SNSSTVAIDHSLSLAG-ERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVL EVINSSTEGLILNIDKDIRKILSGYIVEIEDTEGLKEVINDR-YDMLNISSLRODGKTFI Query Match
4.7%; Score 178; DB 1; Length 1302;
Best Local Similarity 18.0%; Pred. No. 0.33;
Matches 138; Conservative 141; Mismatches 285; Indels 20: DFKKYNDKLPLYISNPNYKVNVYAVT----KENTIINPSENGDTST 718 AKESLDAKVTEITKKLETFNKDKDVKFKELEKTRKDIDEFINTNKTNP-<u>:</u> 969 327 772 913 561 989 878 998 677 386 441 176 536 169 217 744 825 501 8 8 셤 à 원 & 8 6 A 8 B 8 8 B ద 8 6 ð g 8 P ò qq ð ò

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hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 R;Bolotin, A.; Windker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Genome Res. 11, 731-753, 2001 A;Aillon, O.; Malarme, K.; Weissenbach, J.; Ehrl A;Reference number: A86625; MUD:21235186; PMID:11337471 hacterium Lactococcus lactis s A;Accession: A86827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 NKBLFBOYKEBVTVLLNKYYAVELKNKFD-KTKNDSKOIIKEIKDAHNYCTLESGKSEKK 1079
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                                                                                                                                                                                                                                                                                                                                                               637 KILSGYIVEIEDT-----EGLKEVINDRYDMLNISSLRODGKTFIDFKKYNDKLPL 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTŞRTHTSEVHGNAEVH----A 311
                                                                                                                                                                                                                                                                                                                                                                                                                         EKKG-----LIKYKSSPEKWSTASDPYSDFEKVTG------RIDKNVSPEARHPL
                                                                                                                                                                                                                                                                 LKHYDF-----SDFGKEGNIKYTDKIKKINDDIMAVSQQIDQHINGLDDIQKKSES
                                                                                                                                                                                                                                                                                                                              -LPELKOKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   974 KSQYILEIKKNNGT---NDHDYNIKELK-SHKDKSNGYK-TEADQNKKAIQK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MN-----ILIRDKRFHYDRNNIAVGADESVVKEAHREVIN----SSTEGLLLNIDKDIR
                                                                                                                                        NQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDD-----QEVINKASNSNKIRLEK
                                                                                                                                                                      DIYDKSSKIIQDFSR-ESDINDIKNKLO------KNVSESQNHNSDINQCLNEV
                                             1 EVKQENRL----LNESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSE
                                                                                        QTKLENKFTEFSLNNHEANNNELI-KYPSDLKANLGINEENMLYNOFTEKEKTFNDIKEK
                                                                                                                                                                                                                                   111 GRLYQIKIQYQRENPIEKGLDFKLYWTDSQNK------KEVISSDNLQ----
Gaps
178;
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Indels
Mismatches 339;
  Conservative 152;
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A;Molecule type: DNA
A;Residues: 1-1072 <ST
     156;
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A,Cross-references: EMBL:127838; NID:9457145; PID:9457146; PIDN:AAA21304.1
R,Cross-references: EMBL:127838; NID:9457145; PID:9457146; PIDN:AAA21304.1
R,Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
R,Cochem. Parasitol. 42, 241-246, 1990
A,Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple A,Reference number: A45521; MUID:91101660; PMID:2270106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of Plasmodium yoelii
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                                                                                                                                                                 ------KRFDTSDESLKWELSNVKV-- 266
                                                                                                                                                                                                                                                               -----TEROSKKSENDASAFS-GNSLVSKFNSLKND----DEKIKLLES---VFVFDLK 312
                           ---KRIFLSPWISNIHEKK---GLTKYKSSPEKWSTASDPY 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28677; C4527.
B;Keen, J.; Sinha, K.; Brown, K.; Holder, A.
Mol. Biochem. Parasitol. 65, 171-177, 1994
A;Title: A gene coding for a high molecular mass rhoptry protein of Plasmodi
A;Reference number: Z20508; MuID:95021522; PMID:7935623
                                                                                                                                                                                                                                                                                                                                                                                                                                      364 SLFRPS----SKESTILITGLKEELSREKLINSIVDKVELKWTSKDAID-KILASTITSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YDRINII AVGADESVVKEAHREVINSSTEGLLLINI DKDIRKILSGYIVEIEDTEG-LKEVI
                                                                      183 DDKAVEKNISENTEFDVELKTENNAFVGGYSNDIAGTKVIEAIVKYKANSEK-----Y
                                                                                                                         234 SDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNT
                                                                                                                                                                                                                 STSRIHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLN
                                                                                                                                                                                                                                                                                                               TADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTL------ATIDADE---NOLS
                                                                                                                                                                                                                                                                                                                                                          313 TNENTKLSYKYRDIK-----FNKLET---VEGOKGSVKLTYLIGWKVVDGNESIPNRLT
                                                                                                                                                                                                                                                                                                                                                                                                            QILAPNNYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 NDRYDMLNISSLRQDG-KTFIDF-----KKYNDKLP-----LYISNPNYKVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSINREDNEMFEYKIIEPKDDKNAD-DKNGSLKIMVSLSYKNTKFSK 716
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A,Molecule type: DNA
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Pred. No. 0.53;
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Molecule type: DN
Residues: 2131-2269 <KE2>
(Cross-references: GB:M34283
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Best Local Similarity
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Qy 385 LGKW-QTLATIDAD-ENQLSQILAPNNYYPSKNLAPIALNAQKKF 427	Qy 286 TRIISKNTSTSRTHTSEVHGNAEVHASPPDIGGSVSAGFSNSNSSTVAIDHS 337 Qy 2720 LATAXQAAKOALRQMTHLSDAQKQSITGQIDSATQVTGVQSVKDNATNLDNA 2771
Qy 428 SSTPITMAYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSE 479 : : : : : :	OY 338 LSLAGERTWAETWGLNTADTARLNANIRYNNTGTAPIYNVLPTTSLV 384
QY 480 VLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTK 518	Qy 385 LGKNQTLATIDADENQLSQILAPNNYYPSKNLAPIALNAQKKFSSTPITMYN-QF 439 Db 2828 QAANQVNTNKTALNGAQNLANKKQETTANINRLSHLNNAQKQDLNTQVTNAPNIST 2883
QY 519 PDWTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIY 575	440 LELEKT : 2884 VNQVKT
QY 576 TVLDKIKUNAKANILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLINIDK 633	OY 467 GRURYDIGSNWSEVLPQIQE-TTARIIFNGKDLNLVERRIAAVNPSDPLET 516 DD 2944 GTNANQSQVEAALSTVTTTKQALNGDRKVTDAKNNANQTLSTLDNLNNA 2992
QY 634 DIRKILSGYIVEIEDTEGIKEVINDRYDMLNISSLRQDGKTFIDFKKYND 683	QY 517TKPDMTLKEALKIAFGFNEPNGNLQYQGKDITBFDFNFD 555 :-
Qy 684 KLPLYISN-PNYKYNVYAVTKENTIINPSENGDISTNGIKKILIFSKK 730 1070 -INTYFKNAEEYNQNVSLNFNNIEMADTKSQYILNIKKNNGTNNTDYNIKELKEHKKK 1126	Qy 556QQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESV 611 :
RESULT 10 B89921	Qy 612 VKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISS 667
ct-2001 i, I.; Cui, L.;	668
cimi	RESULT 11
A,Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A,Reference number: A89758; MUID:21311952; PMID:11418146 A,Accession: B89921 A,Status: preliminary	07 7030 [imported] - Mycoplasma pulmonis (strain UAB CTIP) Ilmonis puence_revision 24-May-2001 #text_change 03-Aug-2001
A,Molecule type: DNA A,Rolecule type: DNA A,Residues: 1-6713 «KUR» A,Cross.references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149 A,Experimental source: strain N315 C;Genetics: A,Gene: ebbA	Richambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I. Nucleic Acids Res. 29, 2145-2153, 2001 A; Fitle: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul A; Reference number: A99512; MUID:21267165; PMID:11353084 A; Accession: G90599
Query Match Best Local Similarity 20.4%; Score 182; DB 2; Length 6713; Best Local Similarity 20.4%; Pred. No. 2.3; Matches 170; Conservative 133; Mismatches 298; Indels 232; Gaps 44;	A,Scalus: Preiminary A,Molecule type: DNA A,Residues: 1-752 «KUR» A,Cross-references: GB:A1445566, PID:g14090118; PIDN:CAC13876.1; GSPDB:GN00153 A.Experimental source: strain UAB CTIP
Qy 9 INESESSOGILGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA 63 :::: :: :	C;Genetics: A;Gene: MYPU 7030 A;Genetic code: SGC3
Qy 64 IWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKI 118	Query Match Best Local Similarity 19.5%; Pred. No. 0.1; Matches 161; Conservative 129; Mismatches 269; Indels 268; Gaps 43;
OY 119 QYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGP 173 Db 2577 AIQSVTSTENALNGDANLQCAKTEATQAIDNLTQLNTPQKTALKQQVNAAQR 2628	Qy 41 GDLSIPSSELENIPSENQYPQSAIWSGFIKVKKSDEYTFATSADNHVTWMVD 92
Qy 174 TVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKGSPEK 225	QY 93 DQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQ 140 :: :: :: :: :: ::
226 WSTASDPYSDFEKVTGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE 226 WSTASDPYSDFEKVTGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE 2273 QGAYTDAYNAAKNIVNG-SPNVITNAADVTAATQRVNNAETSLNGDTN	QY 141 NKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTV 194 -
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Db 1186 INLSDI-NIFDNITKSVTYNILINAQKGITGISGANGYEKILFYGMKIQNATYSDNNNIQT 1244 Qy 606 GADESVVKEAHRBVINSSTEGILLANIDKDI	TESTIL 9 THE STATE OF COLOUR PORTING (ITEGEMENT) THE STATE OF COLOUR PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE STATE PORTING STATE
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  PIDN:CAC13866.1; GSPDB:GN00153
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                                                                                                                                                                                  AIWS-----GFIKV------KKSDEYTFATSADNHVTMWVDDQE----VI
                                                                                                       Gaps
                                                                                                       207;
                                                                            Length 1125;
                                                                                                      Indels
                                                                                                                                                                                                                                     NKASNSNKIRLE-----KGRLYQIKIOYQRENPTEKGL--
                                                                             5.1%; Score 191.5; DB 2;
llarity 19.2%; Pred. No. 0.055;
Conservative 163; Mismatches 328;
A,Cross-references: GB:AL445566; PID:g14090108; A,Experimental source: strain UAB CTIP C,Genetics:
A,Genet: MYPU 6930
A,Genetic code: SGC3
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RESULT S05603

gene from 1410 1465 1020 1076 576 1077 T-----KGLVKYYNGESSPLK 1103 437 47; 223 965 63 LKEVİKNKN---YTGNSPSENNT------DVNNALESYKKFLPEGTDVATVVS 1370 DSID-----TDINFA------NDVLGYYKILSEKYKSDLDSIKKYINDKQGE -----QFLELEKTKQLRLDTDQV-YGNIAT-----YNFENGRVRVDTGSNWSEVL ----ETTKPDM-TLKEALKIAFGF -----FDFNFDQQTSQNIKNQLAELNATNIYT MENIILSKNEDQSTQNTDSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS -SLVLGKNOTLATIDADENOLSQILAPNNYYPSKNLAPIA---LNAQKKFSSTPITWNYN SET STATE ST ----QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS 1021 KKKTVGKYKMQIKKITLLKEQLESKL--NSLNNPKHVL--QNFSVFFNKKKEAEIAETEN NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTT-------YEKILKDSDTFYNE TSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKY---KSSP-----EKWSTASDPYSDFE-----KVTGRIDKNVSPEAR-------HPLVAAYPIVHVD 09-Jun-2000 A;Cross-references: EMBL:X15063 C;Superfamily: major merozoite surface antigen C;Reywords: glycoprotein; merozoite; surface antigen E;1-19/Domain: signal sequence #status predicted <SIG> F;20-1639/Product: major merozoite surface antigen #status predicted <MAT> ENRL-LINESESSOGLLGYYFSDLNFOAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA 64 IWSGFIKVKKSDEYTFATSADNHVTMMVDDQEVINKASNS-----NKIRLBKGRLY-RiMyler, P.J.

Nucleic Acids Res. 17, 5401, 1989

A;Tille: Nucleotide and deduced amino acid sequence of the gp195 (MSA-1)

A;Tille: Nucleotide and deduced amino acid sequence of the gp195 (MSA-1)

A;Reference number: S04850; MUID:89345116; PMID:2668887 RiMyler, D.J.
submitted to the EMBi Data Library, April 1989
A;Reference number: 805603
A;Accession: 805603
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-1639 < MYLL>
A;Cross-references: EMBL:X15063; NID:g9896; PIDN:CAA33163.1; PID:g9897 Length 1639; #text_change Indels - malaria parasite ENILSLGKOKONIYQELIGQKSSE-NF--------Query Match
Best Local Similarity 20.6%; Pred. No. 0.11;
Matches 171; Conservative 138; Mismatches 255; major merozoite surface antigen precursor - malaria N;Alternate names: gpl95 surface antigen C;Species: Plasmodium falciparum C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 . C;Accession: S05603; S04850 POIQETTARIIFNGKDLNLVERRIAAVNPSDPL---NEPN----GNLQYQGKDITE----A; Molecule type: mRNA A; Residues: 1504-1639 < MYL2> Accession: S04850 266 1157 1201 1257 1311 1411 382 534 326 438 482 224 1104 m 115 169 g g $\dot{\delta}$ ద Š g ò g ò a ò 셤 임 유 ò g ઠે ઠે ò ò

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membrane nuclease, lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: E90598
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pul
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: E90598
A;Accession: E90598
A;Accession: preliminary
A;Molecule type: DNA
A;Residues: 1-1125 <KUR>
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   Gaps
   186;
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   174; Conservative 131; Mismatches 325;
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A;Reference number: A59091; MVID:99445483; PMID:10515943
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Local Similarity 34.6%; Pred. No. 2.6e-05;
Les 56; Conservative 36; Mismatches 47;
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QY 60 FQSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQ 119	QY 120 YQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTS 170	QY 171 AGPTVP	OY 212 EKKGLTKYKSSPEKWSTASDPYSDFEKYTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL 271 : : : : :	OY 272 SKNEDGSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSST 331	QY 332 VAIDHSLGLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSL 383 : : : : : : : : : : : : : : : : : : :	OY 384 VLGKNOTLATIDADENQLSQILAPUNYYPSKNLAPIALNAQKKFSSTPITWNYNQFLELE 443	OY 444 KTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVER 503	OY 504 RIAAVNPSDPLETTRPDWTLKBALKIAFGFNEPNGNLOY-QGKDITEFDFNFDQQTSQ 560 :	QY 561 NIKNQLAELNATNIYTVLDKIKLNAKOMILIRDKRFHYDR-NNIAVGADESVVKEAHR 617	Qy 618 EVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVIND 658 :	Qy 659 RYDMLNIS	Qy 697NVYAVTKENTIINPSENGDISTNGI 721 Db 760 ILDAHNKYYADIKLDTNTGNTYIDGI 785	5-Oct-1999	R;Welkos, S.L.; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J. Gene 69, 287-300, 1988 A;Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthx A;Reference number: 139933; MUID:89172073; PMID:3148491 A;Accession: 139933	A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: DNA A,Residues: 1-192 <res> A,Cross-references: GB:M22589; NID:g143280; PIDN:AAA22636.1; PID:g143281</res>	Query Match 6.2%; Score 235.5; DB 2; Length 192; Best Local Similarity 34.6%; Pred. No. 2.4e-05; Matches 56; Conservative 36; Mismatches 47; Indels 23; Gaps 6;
OY 61 QSAIWGGFIKVKKSDEYTPATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120 	Qy 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180	Qy 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGL/RKYKSSPEKWSTASDPYSDFEKVT 240	OY 241 GRIDKNVSPEARHPLVAAXPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTSRTHT 300 270 GRIDKNVSPEARHPLVAAXPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTSRTHT 329	QY 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360	Qy 361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIDADENQLSQILAPNNYYPSKNLAPIA 420 	OY 421 INAOKKESSTPITMONOFLELEKTKOLRLDTDOVYGNIATYNFENGRVRVDTGSNWSBV 480	OY 481 LPQIQETTARIIENGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540	Qy 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKANILIRDKRFHYDR 600	Cy 601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDFEGLKEVINDRY 660	Qy 661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720	Qy 721 IKKILIFSKKGYBIG 735	RESULT 2 140862 iota toxin component 1b - Clostridium perfringens	C;Species: Clostinaum Parithingens C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999 C;Accession: 140862; S42774 R;Perelle, S.; Gibert, M.; Boquet, P.; Popoff, M.R. Infect. Immun. 61, 5147-5156, 1993 A;Title: Characterization of Clostridium perfringens iota-toxin genes and expression in A;Reference number: 140861; MID:94041637; PMID:8225592	A; Accession: 140862 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Molecule type: NA A; Cross-references: TMBL; X73562; NID: G929031; PIDN: CAA51960.1; PID: G414655	gth 875; ndels 150; Gaps	QY 1 EVKQENKLINESESSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIFSSELENIPSE-NQY 59 : :

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

May 3, 2004, 19:30:47; Search time 13.0855 Seconds (without alignments) 5403.004 Million cell updates/sec

US-09-848-909A-11 3774 1 EVKQENRLINESESSSQGLL......TSTNGIKKILIFSKKGYEIG 735 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	sctive antige	iota toxin compone	cryptic protein -	hypothetical prote	hypothetical prote	ane nucl	major merozoite su	toxin-like outer m	rhoptry protein -	hypothetical prote	hypothetical prote	rhoptry protein -	Pro Dr	surface-located me	Ω	2	o	major merozoite su	_	toxin-like outer m	_	L D	٠,	hypothetical prote	chetical	protein homo	ell surface anti	а Б	hypothetical prote
SUMMARIES	ID	I39934	I40862	I39933	G59104	F82885	E90598	805603	B64635	T28676	B89921	690299	T28677	A86827	JC6009	T31105	JQ0894	C97033	SAZQK1	AI0452	H71879	568218	S55101	S55805	T18469	S67087	SS6850	B71704	T31102	F82884
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169	168	166.5	166	165	165	164.5	164.5	164	164	164	164	163.5	163	163	163
30	31	32	33	34	35	36	37	38	39	40	4.1	42	43	4	45

ALIGNMENTS

protective antigen precursor - Bacillus anthracis plasmid
C.)Decles: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 01-Dec-2000
C;Accession: I39934; S69160; F59104 R;Welkos, S.L.; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J.
Gene 69, 287-300, 1988 A:Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthr
A, Reference number: I39933; MUID:89172073; PMID:3148491
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: GB:M22589; NID:g143280; PIDN:AAA22637.1; PID:g143282 P:Priedman T C : Gordon V M : Leppla, S.H.: Klimpel, K.R.; Birch, N.P.; Loh, Y.P.
A,Title: In vitro processing of anthrax toxin protective antigen by recombinant PC1 (SF) a.Peference number: S69160: MIID:95142670; PMID:7840657
A, Accession: S69160
A, Molecule type: protein
A; restauces: 127-202 chr. Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle R; Øktinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle
J. Bacteriol. 181, 6509-6515, 1999
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A Accession: F59104
A;Status: preliminary
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A. Cross-references: GB:AF065404, NID:g4894216; PIDN:AAD32414.1; PID:g4894326
o anthrax toxin molecy, proceddive amelyen, paya tormeily pas,
A;Gene: pX01-110
A;Genome: plasmid
to receptors on
edema factor or lethal factor; the complex is internalized
C; Keywords: exotoxin
P;1-29/Domain: signal sequence #status predicted <sig></sig>
F;30-196/Domain: propeptide #Btatus predicted <fku> F;197-202/Product: protective antigen #status experimental <mat></mat></fku>
99.3%;
Best Local Similarity 99.5%; Pred. No. 2.3e-182; Matches 731; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

480 540

420 420

300 300 360 360 999 720 720

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LNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480
                                                                                                                                                                                                                                   DMINISSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                                   NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIDADENQLSQILAPNNYYPSKNLAPIA
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DGI PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLIKYKSSPEKWSTASDPYSDFEKVT
                                           GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT
                                                       GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDGSTQNTDSETRTISKNTSTSRTHT
                                                                                     SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
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Sequence 6, Application PC/TUSO335733

Sequence 6, Application PC/TUSO335733

SEQUENCE INFORMATION:
TOTALE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/USO3/35733
CURRENT PILING DATE: 2003-10-06
PRIOR PILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 735
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Pred. No. 2.4e-296;
0; Mismatches 4;
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Best Local Similarity 99.5%;
Matches 731; Conservative
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PCT-US03-35733-6
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TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00142/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: 9044,987
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
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99.3%; Score 3749; DB 1;
Best Local Similarity 99.5%; Pred. No. 2.4e-296;
Matches 731; Conservative 0; Mismatches 4;
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ORGANISM: Bacillus anthracis
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Sequence 7, Application US/09848909A
GENERAL INFORMATION:

APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT FILING DATE: 2001-05-04
PRIOR PLING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FREESEQ for Windows Version 4.0
: SEQ ID NO 7:
LENGTH: 735
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Similarity 99.5%; Pred. No. 2e-2
11; Conservative 1; Mismatches
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ORGANISM: Bacillus anthracis
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LNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
                 LPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
APPLICANT: President and Pellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFRENCE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: DC 60/424,987
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR PILLING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FRSELEQ for Windows Version 4.0
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Pred. No. 2e-296;
1; Mismatches 3;
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Local Similarity 99.5%;
les 731; Conservative 1
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PCT-US03-35733-7
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Sequence 13, Application US/09848909A

GENERAL INFORMATION:
APPLICANT: Collier, R. John
ITLE OF INVENTION: Compounds and Methods for the Treatment
ITLE OF INVENTION: Compounds and Methods for the Treatment
ITLE OF INVENTION: Compounds and Methods for the Treatment
ITLE OF INVENTION: ORDER: US/09/848,909A

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT FILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 13
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Pred. No. 1.1e-296;
0; Mismatches 3; Indels 0
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Best Local Similarity 99.68;
Matches 732; Conservative
                                                                                                                                                                                                                                                                                                  IKKILIFSKKGYEIG 735
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US-09-848-909A-13
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Best Local Similarity 99.6%;
Matches 732; Conservative
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PCT-US03-35733-13
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                           DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                               DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: COMPOUNDER: US/09/848,909A
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR PRIOR PLING DATE: 2000-05-04
NUMBER: OF SEQ ID NOS: 35
SOSTWARE: FREESEQ for Windows Version 4.0
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Pred. No. 9.5e-297;
0; Mismatches 3;
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Best Local Similarity 99.6%;
Matches 732; Conservative (
                                                                                                     IKKILIFSKKGYEIG 735
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PGT-US03-35733-13
FGT-US03-35733-13
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT PILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 735 Length 735; Indels Score 3753; DB 1; Pred. No. 1.1e-296; 0; Mismatches 3;

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QSAIWSGFIKVKKSDEYTFATSADNHVIMMVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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Sequence 8, Application PC/TUS0335733
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 735
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99.5%; Score 3754; DB 1;
Best Local Similarity 99.6%; Pred. No. 9.5e-297;
Matches 732; Conservative 0; Mismatches 3;
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                                                                   GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: Colliar, R. John

APPLICANT: Calliar, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: and Prevention of Bacterial Infection

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PASICE OF WINDOWS VERSION 4.0

LENGTH: 735
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Pred. No. 7.9e-297;
0; Mismatches 3;
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(1 Similarity 99.6%;
732; Conservative
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Best Local S:
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; Sequence 2, Application PC/TUS0335733
; GENERAL INFORMATION:
    APPLICANT: President and Fellows of Harvard College et al.
    ITILE OF INVENTION: Compounds and Methods for the Treatment
    ITILE OF INVENTION: Compounds and Methods for the Treatment
    ITILE OF INVENTION: and Prevention of Bacterial Infection
    FILE REFERENCE: 00742/072003
; CURRENT APPLICATION NUMBER: PCT/US03/35733
; CURRENT FILING DATE: 2003-10-10
    PRIOR APPLICATION NUMBER: US 60/424,987
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                     Score 3755; DB 1;
Pred. No. 7.9e-297;
0; Mismatches 3;
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Best Local Similarity 99.6%;
Matches 732; Conservative
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        TITLE OF INVENTION: Modified Shine Dalgarno Sequences and Methods of Use Thereof FILE REFRENCE: PV595PCT
CURRENT APPLICATION UNMBER: PCT/US03/19786
CURRENT FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 18
SSO TAMAE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 735
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Best Local Similarity 99.6%; Pred. No. 4.5e-297;
Matches 732; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Mature PA sequence including an
PCT-US03-19786-4
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Pred. No. 2.5e-297;
0; Mismatches 2;
                                                                 Version 4.0
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PCT-US03-19786-4
; Sequence 4, Application PC/TUS0319786
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/20
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: RestSEQ for Windows Vers
SEQ ID NO 10
LENGTH: 735
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Best Local Similarity 99.7%;
Matches 733; Conservative (
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                                                                                                 Score 3761; DB 1;
Pred. No. 2.5e-297;
0; Mismatches 2;
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GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the
TITLE OF INVENTION: and Prevention of Bacterial
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
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Conservative
                                                      anthracis
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                                     r TYPE: PRT
CORGANISM: Bacillus
PCT-US03-35733-10
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                                                                                                                    Best Local Simi
Matches 733;
      SEQ ID NO 10
LENGTH: 735
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                           EVKQENRILNESESSSQGLIGYYFSDINFQAPWVVTSSTTGDLSIPSSELENIPSENQYF
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Sequence 11, Application US/09848909A

SEQUENCE INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: and Prevention of Bacterial Infection

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT APPLICATION NUMBER: US 60/201,800

PRIOR FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11
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ORGANISM: Bacillus anthracis
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Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli Sequence 13, Appl Sequence 13, Appl Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 19, Appli Sequence 20, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli

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100.0%; Score 3774; DB 1; Length 735; 100.0%; Pred. No. 2.2e-298; ive 0; Mismatches 0; Indels 0;
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Sequence 11, Application PC/TUS0335733
GENERAL INFORMATION:
TOTHER TOTHER PRESIDENT OF THE PROBLEM OF HARVARD COllege et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 07742/07203
CURRENT APPLICATION NUMBER: 9C 60/424,987
FRIOR APPLICATION NUMBER: US 60/424,987
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FRSEE FOR Mindows Version 4.0
SEQ ID NOS: 38
LENGTH: 735
                                                                                             PCT-US03-19786-4

PCT-US03-19786-4

BCT-US03-15733-2

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Sequence 14, Application US/09848909

Sequence 14, Application US/09848909

Publication NO. US20020039588A1

APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection

FILE OF INVENTION: and Prevention of Bacterial Infection

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

PRIOR PRIOR DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: BastSEQ for Windows Version 4.0

LENGTH: 736
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Score 3748; DB 12;
Pred. No. 5.1e-273;
0; Mismatches 4;
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                               QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                               DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/06002
CURRENT APPLICATION NUMBER: US/09/848,909
FRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASESEQ for Windows Version 4.0
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Pred. No. 5.1e-273;
0; Mismatches 4;
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US-09-848-909-13
US-09-848-909-13
Sequence 13, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
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Best Local Similarity 99.5%;
Matches 731; Conservative
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Sequence 12, Application US/09848909

Sequence 12, Application US/09848909

Sequence 12, Application US/0988A1

GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 0742/06002

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT PILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FatlSEQ for Windows Version 4.0

SEQ ID NO 12.
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Pred. No. 5.1e-273;
0; Mismatches 4;
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Best Local Similarity 99.5%;
Matches 731; Conservative (
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                                          481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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Publication No. US20020039588A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THEORIEM COllier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: DEPORTED ON COMPOUNDS:
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
PRIOR FILING DATE: 2000-04-04
SOFTWARE: PSECSO for Windows Version 4.0
SEQ ID NO 9
LENGTH: 736
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Pred. No. 5.1e-273;
0; Mismatches 4;
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ilarity 99.5%;
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; ORGANISM: Bacillus anthracis
US-09-848-909-9
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Best Local Simil
Matches 731; C
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Sequence 8, Application No. US2002039588A1

GENERAL INFORMATION:

APPLICANT: Colliar, R. John

APPLICANT: Colliar, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment;

TITLE OF INVENTION: Compounds and Methods for the Treatment;

TITLE OF INVENTION: and Prevention of Bacterial Infection;

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800

PRIOR PRIOR DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PRESEQ for Windows Version 4.0

LENGTH: 736
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Pred. No. 5.1e-273;
0; Mismatches 4;
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Best Local Similarity 99.5%;
Matches 731; Conservative
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CRGANISM: Bacillus anthracis
US-09-848-909-8
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                        DMINISSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                                      DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTINPSENGDTSTNG
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                                                                                                                                                                                                                                                  Sequence 7, Application US/09848909
; Publication No. US2002039588A1
; GENERAL INFORMATION:
; APPLICANT: COllier. R. John
; APPLICANT: Collier. R. John
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                       TYPE: PRT
CRGANISM: Bacillus anthracis
US-09-848-909-7
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Best Local Similarity 99.5<sup>3</sup>
Matches 731, Conservative
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                                                                                                                 Sequence 6, Application US/09848909; Sequence 6, Application US/09848909; Publication No. US20020039588A1; GENERAL INFORMATION:
APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; APPLICANT: Collier, R. John; TITLE OF INVENTION: and Prevention of Bacterial Infection; FILE REFERENCE: 00742/060002; CURRENT APPLICATION NUMBER: US/09/848,909; CURRENT FILING DATE: 2001-05-04; PRIOR FILING DATE: 2000-04-04; PRIOR FILING DATE: 2000-04-04; NUMBER OF SEQ ID NOS: 35; SOFTMARE: PESECRE for Windows Version 4.0
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Matches 731; Conservative
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; TITLE OF INVENTION: and Prevention of Bacterial Infection
; FILE REFERENCE: 00742/060002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR PILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FASISEQ for Windows Version 4.0
; SEQ ID NO 4
; TYPE: PRT
; TYPE: PRT
; ORGANISM: Bacillus anthracis
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RESULT 6 US-09-848-909-5

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Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
TITLE OF INVENTION: US 00002
CURRENT FILING DATE: 2001-05-04
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 736 Length 736; Indels Score 3748; DB 12; Pred. No. 5.1e-273; 0; Mismatches 4; 721 IXKILIFSKKGYEIG 735 Query Match
Best Local Similarity 99.5%;
Matches 731; Conservative ; TYPE: PRT ; ORGANISM: Bacillus anthracis US-09-848-909-5 g ò ö

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                                                                                                                                                                          Score 3748; DB 12;
Pred. No. 5.1e-273;
0; Mismatches 4;
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NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
LENGTH: 736
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al Similarity 99.5%;
731; Conservative
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ORGANISM: Bacillus anthracis
US-09-848-909-3
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US-09-848-909-3

Sequence 3, Application US/09848909

Publication No. US20020039588A1

GENERAL INFORMATION:

APPLICANT: Collier, R. John

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

FILE REPERBNCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800
                                                  Length
                                                                                           Indels
                                                  12;
                                             Score 3748; DB 12;
Pred. No. 5.1e-273;
0; Mismatches 4;
                                                  99.3%;
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; Sequence 2, Application US/09848909
; Publication No. US2020039588A1
; Publication No. US2020039588A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Collier, R. John
; TITLE OF INVENTION: cand Prevention of Bacterial Infection
rILE REFERENCE: 00742/060002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2000-04-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; NUMBER OF SEQ ID NOS: 35 500-04-04
; SEQ ID NO 2: 35 500 10 NO 2: 550 10 NO 2: 550 10 NO 2
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Sequence 1, Application US/09848909

Publication NO. US20020039588A1

GENERAL INFORMATION:

APPLICANT: Collier, R. John

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT PILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800

PRIOR APPLICATION NUMBER: US 60/201,800

PRIOR PRILING DATE: 2000-04-04

SOFTWARE: PRESEQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 736
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 30, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 5, Appli	9	Sequence 7, Appli	8	Sequence 9, Appli	10,	Sequence 11, Appl	Sequence 12, Appl	13,	14.
	ΩI	US-10-410-647-30	US-09-848-909-1	US-09-848-909-2	US-09-848-909-3	US-09-848-909-4	US-09-848-909-5	US-09-848-909-6	US-09-848-909-7	US-09-848-909-8	US-09-848-909-9	US-09-848-909-10	US-09-848-909-11	US-09-848-909-12	US-09-848-909-13	US-09-848-909-14
	DB 1)	12	7	12	12							12	13	12	
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æ	Query Match	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3
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Sequence 15, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 21, Appl Sequence 21, Appl Sequence 23, Appl Sequence 34, Appl Sequence 6, Appli Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appl Sequence 681, Appli Sequence 681, Appli Sequence 681, Appli Sequence 681, Appli Sequence 681, Appli	Sequence 4, Appli Sequence 14, Appl Sequence 22, Appl Sequence 8, Appli Sequence 9, Appli Sequence 24, Appli Sequence 24, Appli Sequence 7, Appli Sequence 7, Appli
US-09-848 US-09-848 US-09-848 US-09-848 US-09-848 US-09-848 US-09-848 US-10-442 US-10-442 US-10-442 US-10-442 US-10-442 US-10-442 US-10-332 US-10-	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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AL IGNMENTS

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APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: PLEXUS VACCINE, INC.
APPLICANT: Extricth, Vsevolod
APPLICANT: Bardner, Andrew
APPLICANT: Denns, Robert
APPLICANT: Denns, Robert
APPLICANT: Denns, Robert
APPLICANT: Denns, Robert
CURRENT APPLICANTON: IMMUNGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME
FILE REPERENCE: PLEXILLO.
CURRENT APPLICATION NUMBER: US 60/373,668
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: US 60/371,256
PRIOR FILING DATE: 2002-04-08
NUMBER OF SEQ ID NOS: 46
SOUTHWARE: PARENTIN VERSION 3.1
SEQ ID NO 30
LENGTH: 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 735;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 99.3%; Score 3748; DB 15; Best Local Similarity 99.5%; Pred. No. 5.1e-273; Matches 731; Conservative 0; Mismatches 4;
Sequence 30, Application US/10410647 Publication No. US20030235818A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Bacillus anthracis US-10-410-647-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 ADENQLSQILAPNNYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 KT-PSLTLKDALKLSYPDEIKEIEGLLYYKNKPIYESSVMTYLDENTAKEVTKQLNDTTG 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 PLESHTVGDPYTDYEKAARDLDLSNAKETFNPLVAAFPSVNVSMEKVILSPNENLS---- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 ----NSVESHSSTNWSYT----NTE-----GASVEAGIGPKGISFGVSVNYQHSET 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 LAGERTWAETMG----LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATID 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -------LLLNID-----KDIRKILSGYIVEIEDTE------GLKE 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 SIRWIGLIQSKETGDFTFNLSBDEQAIIBINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QENRLINESESSSQGLLGYYFSDINFQAPMVTSSTTGDLSIPSSELEN--IPSENQYFQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42 QKQNQ---QKEMDRKGLLGYYFKGKDF-SNLTMFAPTRDSTLIYDQQTANKLLDKKQQBYQ 97
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                    Query Match
20.3%; Score 766; DB 2; Length 884;
Best Local Similarity 30.1%; Pred. No. 1.5e-46;
Matches 245; Conservative 129; Mismatches 295; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTIINPSENGDI-SINGIK---KILIFSKKGYEIG 735
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 884 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-044-5
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Search completed: May 3, 2004, 19:42:45 Job time : 18.0986 secs

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711 VNKDNYKRLDIIAHNIKSNPISSLH------IKTNDEITLFWDDISI-TDVASIKPE 760
     569
                                   VINDRYDMLN------ISSLRQDGKTFIDFKKYNDKLFLYISNPNYKVNVYAVTKE
                                                                                                  ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                        599 KFKDVSHLYDV----KLTPKMNVTIK-LSILYDN---AESNDNSIGKWTNTNIVSGGNNG
  516 TTKPDMTLKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Macrael, Gragory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Destichka, N. Kristy
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
OCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                         627 ------LLLMID-----KDIRKILSGYIVEIBDTE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM
OPERATING SYSTEM
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
FRICA APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 25-MAR-1994
PRIOR APPLICATION DATA: US 08/037,057
FILING DATE: 25-MAR-1994
PRIOR APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1994
PRIOR APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: PACC, GATY M.
REGISTRATION NUMBER: GC 1695/CIP3/DIV6 - SQLV3
TELEROMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08471044
Patent No. 5840868
GENERAL INFORMATION:
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CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 SD.-İKFNIDSKIFKELKLEKIDSQNQODELRNPERNKKESQBFLAKPSKINLFT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLIKYYKSS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 QXMKREIDED----TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 PEKWSTASDPYSDPEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283 DSETRIISKNISTSRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----NSVESHSSTNWSYT----NTE-----GASVEAGIGPKGISFGVSVNYOHSET 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADENQLSQILAPNNYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 SIRWIGLIQSKETGDFTFNLSEDEQALIEINGKIISNKGKEKQVVHLEKGKLVPIKIBYQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 OKNO---OKEMDRKGLLGYYFKGKDF-SNLTMFAPTRDSTLIYDQQTANKLLDKKQQBYQ 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 QENRLINESESSSQCLLGYYFSDLNFQAPMVVTSSTTGDLSIPSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 884;
                                                                                                            OPERATING SYSTEM: PC-LOS/MS-LOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,033
FILING DATE: US/08/471,033
FILING DATE: US/08/314,594
FILING DATE: US 08/314,594
FILING DATE: US 08/314,594
FILING DATE: US 08/314,594
FILING DATE: US 08/319,018
FILING DATE: US 08/218,018
FILING DATE: US 08/218,018
FILING DATE: US 08/218,018
FILING DATE: US 08/218,018
FILING DATE: US 08/218,018
FILING DATE: S-MAR-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SQLv3
TELEPHONE: 919-541-8689
TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
20.3%; Score 766; DB 1; Length 88;
Best Local Similarity 30.1%; Pred. No. 1.5e-46;
Matches 245; Conservative 129; Mismatches 295; Indels
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
TOPOLOGY: 117-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-08-471-033-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             484
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713 NGDT-STNGIK---KILIFSKKGYEIG 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NO. 5770696el Pe
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GRIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 5, Application US/08471033 ; Patent No. 5770696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Hawthorne STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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Best Local Similarity 30.1%; Pred. No. 1.1e-46;
Matches 243; Conservative 134; Mismatches 300; Indels 130; Gaps 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muller. Cohn, Judy Stamp, Lisa Morrill, George INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORK:
MEDIUTER READABLE FORK:
MEDIUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFFICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
FILING DATE: 06-MAY-1999
FILING DATE: 30-0CT-1997
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
APPLICATION NUMBER: US 60/029,848
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-708CD1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE: PS177C8

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-850-351A-32
764 IKOIYSRYGIKLEDGILIDKKGGIHYG 790
                                                                                                                                                                                                                                               Loewer, David
Dullum, Charles Joseph
                                                                                                                                              APPLICANT: Feitelson, Jerald S. Schnepf, H. Brnest Narva, Kenneth E. Stockhoff, Brian A. Schmeits, James
                                                                                        Sequence 32, Application US/09850351A Patent No. 6656908 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 881 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 352-372-5800 INFORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SD
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                                                                                                                                                                                                                                                                                                                                            TITLE OF
                                                                      US-09-850-351A-32
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321 ----NSVESHSSTNWSYT----NTE-----GASVEAGIGPKGISFGVSVNYQHSET 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 AKSNSTALNISPGESYPKKGONGIALISMDDFNSHPITLNKKGVDNLLNNKPMALETNQT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 ADENQLSQILAPINIYYPSKNLAPIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 YGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           537 KT-PSLTLKDALKLSYPDEIKÉIEGLLYYKNKPÍYÉSSVMTYLDENTAKEVTKÓLNDTTG 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      627 ------LLLNID-----KDIRKILSGYIVEIEDTE------GLKE 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              648 KKQYSSNNPDANLTLNTDAQEKLNKARDYYISLYMKSEKNTQCEITIDGEIYPITTKTVN 707
                                                                                            122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162
                                                                                                                                                                                                                                                                                163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLIKYKSS 222
95 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        481 DG---VYKIKDTHGNIVTGGEWRGVIQQIKAKTASIIVDDGE-RVAEKRVAAKDYENPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               596 KPKDVSHLYDV----KLTPKONVTIK-LSILYDN---AESNDNSIGKWTNTNIVSGGNNG
                                                                                                                                                                                    155 SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPEFNKKESQEFLAKPSKINLFT
                                                                                                                                                                                                                                                                                                                                                                             213 OKMKREIDED----TDTDGDSIPDLWEENGYII-----ONRIAVKWDDSL-ASKGYTKFVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 TTKPDMTLKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Wallins, Martha A
APPLICANT: Wolfors
APPLICANT: Wolfors
APPLICANT: Dead, Nalin M
APPLICANT: Dead, Nalin M
APPLICANT: Carr, Brian
APPLICANT: Carr, Brian
APPLICANT: Carr, Man J
APPLICANT: Estruch, Juan J
APPLICANT: Estruch, Juan J
APPLICANT: Estruch, Juan J
APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
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APPLICANT: SETUCH, Juan J
APPLICANT: SETUCH, Juan J
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                          596 KPXDVSHLYDV ----KLTPKMNVTIK-LSILYDN ----AESNDNSIGKWTNTNIVSGGNNG 647
                                                                                                                                                                                                                                                                                                                                                                                        YGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 515
                                                                                     TTKPDMTLKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL-- 569
                                                                                                                  ---NATNIYTVLDKIKLNAKWNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG 626
                                                                                                                                                                                                                                                                        -----LLLINID-----KDIRKILSGYIVEIEDTE------GLKE 654
                                                                                                                                                                                                                                                                                                                 648 KKQYSSNNPDANLTLNTDAQEKLNKNRDYYISLYMKSEKNTQCEITIDGEIYPITTKTVN 707
                                                                                                                                                                                                                                                                                                                                                             VINDRYDMLNI - - SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNYYAVTKENTIINPSE 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Stockhoff, Brian A.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Coewer, David
APPLICANT: Duillum, Charles Joseph
APPLICANT: Muller-Cohn, Judy
APPLICANT: Muller-Cohn, Judy
APPLICANT: Stamp, Lisa
APPLICANT: Morrill, George
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6603063el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCES: Saliwanchik, Liboyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 32606-6669
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
OCMPUTER: ISM PC Compatible
OFFRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     713 NGDT-STNGIK---KILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               764 IKQIYSRYGİKLEDGİLİDKKGĞIHYG 790
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
PRIOR APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
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APPLICATION NUMBER: US 09/073,898
FILING DATE: 05-MAY-1998
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/307,100
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Patent No. 6603063
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20.3%; Score 768; DB 4; Length 881;
Best Local Similarity 30.1%; Pred. No. 1.1e-46;
Matches 243; Conservative 134; Mismatches 300; Indels 130; Gaps
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              TELECONTUNICATION INFORMATION:
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95 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGXIISNKGKEKQVVHLEKGKLVPIXIEYQ 154
                                                       122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162
                                                                                      SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPBFNKKESQEFLAKPSKINLFT 212
                                                                                                                          163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                                 233 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTONT 282
                                                                                                                                                                                                                         283 DSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
                                                                                                                                                                                                                                                                                                           321 ----NSVESHSSTNWSYT----NTE----GASVEAGIGPKGISFGVSVNYQHSET 363
                                                                                                                                                                                                                                                                                                                                               LAGERTWAETMG----LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATID 395
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APPLICANT: Loewer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Miller-Cohn, Judy
APPLICANT: Stamp, Lisea
APPLICANT: Stamp, Lisea
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanti'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              713 NGDT-STNGIK---KILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                764 IKQIYSRYGİKLEDGİLİDKKGĞIHYG 790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09073898
Patent No. 6242669
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.3%; Score 768; DB 3; Length 881;
Best Local Similarity 30.1%; Pred. No. 1.1e-46;
Matches 243; Conservative 134; Mismatches 300; Indels 130; Gaps
                                                                                                                                                                                                  COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,698
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39,355
FR: MA-708C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
REPERENCE/DOCKET WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 881 amino acids
TYPE: amino acid
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                                 Gainesville
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US-09-073-898-32
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34;
SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL 725
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APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schneff, Brian A.
APPLICANT: Schneits, James
APPLICANT: Schneits, James
APPLICANT: Loewer, James
APPLICANT: Loewer, James
APPLICANT: Willer-Cohn, Judy
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences which Encode These Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCES: 134
APPLICANT: APPLICANT: Sequences which Encode These Toxins
APPLICANT: APPLICANT: Sequences Wilch Encode These Toxins
                                 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,780 FILING DATE: 30-OCT-1997
CLASSIFICATION DATE: 06/029,848
PRIOR APPLICATION DATE: 06/029,848
PILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REGISTRATION NUMBER: 31,794
TELECHONE: 352-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: US
ZIP: 32606-6669
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                            ; Sequence 32, Application US/08960780; Patent No. 6204435
GENERAL INFORMATION:
APPLICANT: Feitelson, Jerald S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; INDIVIDUAL ISOLATE: 177C8
US-08-960-780-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 881 amitory
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amino acid
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                                                                                         726 IFSKKGYEIG 735
                                                                                                                                  269 IFSKKGYEIG 278
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CITY: Gainesville
STATE: FL
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  999
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                                                                                                                                                                                          361 TARLINANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATKAKENQLSQILAPINYYPSKNL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             641 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINFSENGDT 700
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Patent No. 6129156

GENERAL INFORMATION:
APPLICANT: Linino, Nick M
APPLICANT: Lehnert, Bruce E
TITLE OF INVENTION: Receptors
FILE REFERENCE: S-99,662
CURRENT APPLICATION NUMBER: US/09/273,839A
CURRENT APPLICATION NUMBER: US/09/273,839A
CURRENT PILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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    241 EKVIGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTS
                                                                                                     301 RTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD
                                                                                                                                                                                                                                                                                                                                                                            461 WSEVLPQIQETTARIIFNGKDLALVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP
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                                                                      RTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD
                                                                                                                                                             357 TARLMANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIDADBNOLSQILAPNNYYPSKNL
                                                                                                                                                                                                                                                    417 APIALNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN
                                                                                                                                                                                                                                                                                          421 APIALNAÓDDFSSTPITMN------YGNIATYNFENGRVRVDTGSN
                                                                                                                                                                                                                                                                                                                                           477 WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRF
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33.8%; Score 1275; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.5e-84;
Matches 250; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STNGIKKILIFSKKGYEIG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 STNGIKKILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Bacillus anthracis US-09-273-839A-8
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                               641 NDRYDMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTINPSENGDT
  657 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT
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                                                                                                                                                                                                        Sequence 31, Application PC/TUS9401624
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: RILATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: DE PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
SOFTING SYSTEM: PC-DOS/MS-DOS
SOFTIME: PATCHIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 3571; DB 5;
Pred. No. 8.1e-248;
4; Mismatches 9;
                                                                                                                   STNGIKKILIFSKKGYEIG 719
                                                                               STNGIKKILIFSKKGYEIG 735
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NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 152
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 95.0%;
Matches 702; Conservative
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
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PCT-US94-01624-31
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STATE: CA
COUNTRY: USA
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-JUN-1993
CLASS!FICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A:
REGISTRATION NUMBER: 15280-161-1
TELEPHONE: (415) 576-0300
INFORMATION FORWATION:
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 719 amino acids
TYPE: amino acids
TYPE: amino acids
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Pred, No. 8.1e-248;
4; Mismatches 9;
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Best Local Similarity 95.0%;
Matches 702; Conservative
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MOLECULE TYPE: protein
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EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                        ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKOKSSNSRKKRSTSAGPTVPDRDN
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                                                  QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lieppla, Stephen H.
APPLICANT: Rimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Related Methods
ITTLE OF INVENTION: Related Methods
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/08082849B
Patent No. 5677274
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COMPUTER READABLE F
MEDIUM TYPE: Flo
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US-08-082-849B-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALCONIA Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen H. APPLICANT: Arora, Naveen APPLICANT: Arora, Naveen APPLICANT: Alona, Peter J. TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: RELATED METHODS NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSE: TOWNSEND and TOWNSEND KHOURIE and CREW STREET: Steuart Street Tower, 20th Floor, One Market STREET: San Francisco STREET: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA STATE: CA 
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ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPER: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SUSTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATE:

APPLICATION NUMBER: PCT/US94/01624

FILING DATE: June 25, 1993

CLASSIFICATION NUMBER: 1977

ATTORNEY/AGENT INFORMATION:

NAME: Weber: Kenneth A.

REGISTRATION NUMBER: 15280-115

TELEBHOKE/DOCKET NUMBER: 15280-115

TELEBHOKE: (415) 543-9600

TELEBHOKE: (415) 543-9600

TELEBHOKE: (415) 543-5043

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHRACTERISTICS:

LENGTH: 903 amino acids

wver: amino acids
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Best Local Similarity 98.6%;
Matches 724; Conservative
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APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Bighth Floor
GITY: San Francisco
STARTE: California
COUNTRY: USA
ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Datentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-UN-1993
CURRENT APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-UN-1993
ATTORNEY AGENT INFORMATION:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 12-FEB-1993
ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REDERSTRATION NUMBER: 15280-161-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
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                                                                                                                                                                                1; Length 903;
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98.1%; Score 3703.5; DB 1.
Best Local Similarity 98.6%; Pred. No. 3.5e-257;
Matches 724; Conservative 1; Mismatches 6;
                      ; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-021-601-12
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241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300
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181 DGIPDSLEVEGYTVDVRNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                              61 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                               61 QSAIWSGPIKVKKSDEYTFATSADNHYTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
Query Match 98.1%; Score 3703.5; DB 1; Length 903; Best Local Similarity 98.6%; Pred. No. 3.5e-257; Matches 724; Conservative 1; Mismatches 6; Indels 3;
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RESULT 5
US-08-082-849B-12
US-08-080-68 12, Application US/08082849B
; Patent No. 5677274
; GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Arora, Naveen

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                                              241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300
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GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT
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| Sequence 12, Application US/08021601
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Klimpel, Kurt R. |
| APPLICANT: Nichols, Peter J. |
| APPLICANT: Nichols, Peter J. |
| APPLICANT: Angh, Yogendra |
| TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND |
| TITLE OF INVENTION: RELATED METHODS |
| NUMBER OF SEQUENCES: 12 |
| NUMBER OF SEQUENCES: 12 |
| ADDRESSEE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDR
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APPLICATION NUMBER: US/08/021,601
FILING DATE: 19930212
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1414.057
TELECHONICATION INFORMATION:
TELECHONE: 404/688-9880
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: PatentIn Palace
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MEDIUM TYPE: Floppy
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CITY: Atlanta
STATE: Georgia
COUNTRY: USA
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  DMINISSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
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                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Singh, Yogendra APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
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ZIP: 94105

COMPUTER READABLE FORM:
MEDILUM TYPE: Floppy disk
COMPUTER: PER PC compatible
COMPUTER: PER PC compatible
COMPUTER: PAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLEASIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WEBER KENER KENER 31, 677
REGISTRATION NUMBER: 15280-115
REFERENCE/DOCKET NUMBER: 15280-115
TELEPHONE: (415) 549-9600
TELEFRA: (415) 543-9600
TELEFRA: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENER TOWN TOWER SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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ilarity 99.5%; Pred. No. 1.7e-260;
Conservative 0; Mismatches 4;
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Matches 731; Conserv
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MOLECULE TYPE:
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US-08-082-849B-4
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Matches 731;
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                        QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                             61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                        QRENPTEKGLDPKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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Patent No. 5677274

GENERAL INFORMATION:
APPLICANT: Leppla, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
MUMBER OF SEQUENCES: 35
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Two Embarcadero Center, Eighth Floor
California
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COMPUTER READABLE F
MEDIUM TYPE: Flo
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llarity 99.5%; Pred. No. 1.7e-260;
Conservative 0; Mismatches 4;
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version
                                                 SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/082,849B FILING DATE: 25-JUN-1993
CLASSIFICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION: NAME: Weber, Remneth A. REGISTRATION NUMBER: 31,677
REGISTRATION NUMBER: 31,677
REGISTRATION NUMBER: 15280-161-1
TELECHONE: (415) 576-0200
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
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amino acid
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Sequence 31, Appl
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                                                                                      May 3, 2004, 19:31:43 ; Search time 15.0986 Seconds (without alignments) 2513.152 Million cell updates/sec
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Sequence 4, Appl
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3774
1 EVKQENRLINBSESSSQGLL......TSTNGIKKILIFSKKGYEIG 735
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPATE: BM PC compatible
COMPATE: BM PC compatible
COMPATE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,601
FILING DATE: 19930212
CLASSIFICATION: 514
ATORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REGISTRATION NUMBER: 36,016
REGISTRATION INFORMATION:
TELEPHONE: 404,688-7770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 404/688-9880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TYPE: AMINO ACID
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690 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 749
                                                                                                                                                                                                                                                                                                                                                                     Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine; humoral; cell-mediated; immune memory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protecting animal against lethal infection with Bacillus anthracis, by administering wildtype or mutated form of Bacillus anthracis lethal factor protein or its fragment or a nucleic acid encoding the mutated
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/label= Signal peptide
/note= "Not given in the specification"
30. .764
/label= PA
                                                                                                                                                                                                                                                                                                                          Wild type B. anthracis protective antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                           AAB47306 standard; protein; 764 AA
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/label= pCPA
                                        721 IKKILIFSKKGYEIG 735
                                                                    750 IKKILIFSKKGYEIG 764
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N-PSDB; AAC86016.
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Score 3748; DB 4; Length 764; Pred. No. 1.3e-239;

99.3%; 99.5%;

Query Match Best Local Similarity

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390 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQ1LAPNNYYPSKNLAPIA 449
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                                                                 1 EVKQENRILINESESSSQGILGYYFSDINFQAPMVVTSSTTGDLSIPSSBLENIPSENQYF
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         QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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                                                                                                               The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus anthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced with those of tissue plasminogen with its secretory signals replaced with those of tissue plasminogen activator) and PAG3 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as useful for analyzing the effectiveness of drugs and agents that inhibit anthrax or B. anthracis proteins. The present sequence represents a B.
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ubinant DNA construct useful as vaccines for anthrax, in producing cells for analyzing the drugs and agents inhibiting anthrax.
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99.3%; Score 3748; DB 3;
Best Local Similarity 99.5%; Pred. No. 1.3e-239;
Matches 731; Conservative 0; Mismatches 4;
                                                                          Disclosure; Page 33; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                  anthracis PA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 764 AA;
         Recombinant DNA
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Welkos SL;

Smith JF,

Parker MD,

US MEDICAL RES INST INFECTIOUS DISEASES. WPI; 2000-182165/16 N-PSDB; AAZ56875. Pushko P, Sequence 736 AA; Recombinant (USME-) Lee JS,

The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus arthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced with those of tissue plasminogen activator) and RAS3 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as useful for analyzing the effectiveness of drugs and agents that inhibit anthrax or B. anthracis proteins. The present sequence represents a B. anthracis proteins. The present sequence represents a B. anthracis proteins. The present sequence represents a B. anthracis Proteins. for anthrax, in producing inhibiting anthrax. abinant DNA construct useful as vaccines for cells for analyzing the drugs and agents Disclosure; Page 34; 35pp; English

ö 480 540 900 9 541 601 120 121 181 240 241 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360 361 NANIRYVNIGTAPIYNVLPITSLVLGKNQTLATIDADENQLSQILAPNNYYPSKNLAPIA 420 362 NANIRYVNTGTAPIYNVLPTTGLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 421 481 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKOKSSNSRKKRSTSAGPTVPDRDN 180 61 9 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 422 LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 242 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT INAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELBNIPSENQYF EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF OSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT Gaps ő Length 736; Indels 4 Score 3748; DB 3; Pred. No. 1.2e-239; 0; Mismatches 4; 99.3%; Best Local Similarity 99.5 Matches 731; Conservative 361] 482 302 421 481 601 62 121 122 181 182 241 301 61 Query Match d ద g ઠે g à ઠે ò ò ठ 셤 ਨੇ dd ò g ò g à 원

The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus arthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced with those of tissue plasminogen with its secretory signals replaced with those of tissue plasminogen for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agente that inhibit anthrax or B. anthracis proteins. The present sequence represents a B. ö QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120 QSAIWSGFIKVKKSDEYTFATSADNAVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 148 09 89 661 720 721 Recombinant DNA construct useful as vaccines for anthrax, in producing host cells for analyzing the drugs and agents inhibiting anthrax. EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF EVKQENRLLMESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF Gaps 661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG protein; protective antigen; PA; MAT-PA; TPA-PA; activator; PA63; vaccine; anthrax; antibacterial. .. 0 Indels SI; Welkos Score 3748; DB 3; Pred. No. 1.3e-239; 0; Mismatches 4; (USME-) US MEDICAL RES INST INFECTIOUS DISEASES. Smith JF, Disclosure; Page 32; 35pp; English. AAY56960 standard; protein; 763 AA ·; Parker MD, 98US-0092416P. 99.3%; 99.5%; IKKILIFSKKGYEIG 736 IKKILIFSKKGYBIG 735 protein entry) Conservative anthracis TPA-PA protein WPI; 2000-182165/16. (first TPA-PA us anthracis plasminogen Similarity Bacillus anthracis. Pushko P, N-PSDB; AAZ56876. Sequence 763 AA; WO200002522-A2. 10-JUL-1998; Query Match Best Local Simi Matches 731; 25-APR-2000 20-JAN-2000 Н 61 50 721 722 Bacillus AAY56960; Lee JS, tissue RESULT 13 9 ò ઠે 셤 8 8 à 셤

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EVKQENRILINESESSSQGLLGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                         QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                       QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                                   ORENPIEKGLDFKLYWIDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPIVPDRDN
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                                                                                                                                                DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                               QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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tissue plasminogen
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                                                                                                                         DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                               NNIAVGADESVVKEAHREVINSSTEGLILINIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                                                                      DMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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/note= "Wild-type Asp substituted by
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99.3%; Score 3748; DB 5;
Best Local Similarity 99.5%; Pred. No. 1.2e-239;
Matches 731; Conservative 0; Mismatches 4;
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Misc-difference
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Best Local Similarity 99.5
Matches 731; Conservative
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS113 and AAMS1484-AAMS180), especially mitants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. The present sequence is that of the anthrax PA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant B groups (anthrax
y binary A-B toxin of Bacillus
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                                                                                  04-MAY-2000; 2000US-0201800P.
04-MAY-2001; 2001WO-US014372
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The sequence encoding the protective antigen of Bacillus anthracis may be used in the construction of a nucleic acid which encodes a fusion protein comprising the anthrax protective antigen binding domain of the native anthrax lethal factor and a sequence encoding an activity inducing domain of a second protein. The fusion proteins are useful for the specific filling of tumour cells or the killing of cells infected with intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to correct PN field.)
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Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety; A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein.
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                                                                                                                                                             /note= "Wild-type Asp substituted by Asn"
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Pred. No. 1.1e-239;
0; Mismatches 4;
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99.5%;
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                                                           Bacillus anthracis.
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in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
                                                                                                                                          1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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 LNAQEDFSSTPITMNYNOFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
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                                            LNAOKKFSSTPITMNYNOFLELEKTKOLRLDTDOVYGNIATYNFENGRVRVDTGSNWSEV
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Synthetic.
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Pred. No. 5.8e-240;
0; Mismatches 3;
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11 Similarity 99.6%;
732; Conservative
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                        vaccine; mutant; mutein.
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                                         nthrax, PA; protective antigen; antibacterial; p
moiety; A-B anthrax toxin; Bacillus anthracis;
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99.5%; Pred. No. 9.1e-240;
iive 1; Mismatches 3;
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              PA mutant D425E
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B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA
                                                                                                                                                                                                                                                                                              QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
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                                                                                                                                                                                               LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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                                                    ithrax; PA; protective antigen; antibacterial; pore-forming toxin;
moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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Misc-difference 425
/note= "Wild-type Asp substituted by Lys"
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99.6%; Pred. No. 4.9e-240;
live 0; Mismatches 3;
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nes 732; Conservative
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Anthrax PA mutant D425K
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                                                                                                                               Bacillus anthracis.
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moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                     NANIRYVNIGTAPIYNVLPTTSLVLGKNOTLATIKADENOLSOILAPNYYPSKNLAPIA
                                          LNAQKKFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
                                                    LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
                                                                            LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                                                                         LPQIQETTARIIFNGKOLNLVERRIAAVNPSDPLETTKPDMTLKBALKIAFGFNEPNGNL
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                                                                                                                                                          NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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/note= "Wild-type Ly
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moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                                                                                                                                                                                                    99.5%; Score 3755; DB 5; 99.6%; Pred. No. 4.2e-240; ive 0; Mismatches 3;
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in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                                                                                                                          Length 735;
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                                                                                                                                          Score 3774; DB 5;
Pred. No. 2.3e-241;
Mismatches 0;
                                                                                                                                        100.0%; St
Local Similarity 100.0%; Pi
nes 735; Conservative 0;
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AAM51493

AAM51493

01-FEB-2002

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                         Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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                                                                                                                                                                                            "Wild-type Asp substituted by
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Pred. No. 1.7e-240;
0; Mismatches 2;
                                                                                                                              ney Location/Qualifiers
Misc-difference 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page; 77pp; English
                                                                                                                                                                                                                                                                                        04-MAY-2001; 2001WO-US014372
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Best Local Similarity 99.7%;
Matches 733; Conservative
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                                                                                     Bacillus anthracis
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	May 3, 2004, 19:26:27 ; Search time 49.1208 Seconds (without alignments) 4227.791 Million cell updates/sec	act ofevolveritizationmen
OM protein - protein search, using sw model	May 3, 2004, 19:26:27 ;	Title: US-09-848-909A-11 Perfect score: 3774
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1 EVKQENRLINESESSSQGLL......TSTNGIKKILIFSKKGYEIG 735 1586107 seqs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

1586107

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

geneseq11980s:*
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geneseq2201s:*
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geneseq20303as:*
geneseq1203as:* A Geneseq 29Jan04:* 1: geneseqp1980s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SS	Description	94 Anthrax	Anthrax	85 Anthrax		95	0 Anthrax	7 Anthrax	σ	9 Protecti	Aam51483 Anthrax P	3 Ant	Aay56959 B. anthra	m m		Aab47306 Wild type	a	4 Anthrax				Aam51492 Anthrax P	Aam51500 Anthrax P	Aam51499 Anthrax P	Abp71693 B. anthra	
SUMMARIES		AAM51494	AAM51493	AAM51485	AAM51491	AAM51495	AAM51490	AAM51487	AAM51489	AAR60179	AAM51483	AAM51488	AAY56959	AAY56960	AAY56958	AAB47306	ADE65872	AAM51484	AAM51486	AAE18289	AAE35717	AAM51492	AAM51500	AAM51499	ABP71693	
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d	Query Match	100.0	o	99.5	99.5	99.4	99.4	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99.3	99	99.3	99.3	99.3	99.2	99.2	99.1	99.1	99.1	98.9	
	Score	3774	3761	3755	3754	3753	3750	3749	3749	3748	3748	3748	3748	3748	3748	3748	3748	3747	3746	3745	3745	3740	3739	3739	3733	
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Aam51498 Anthrax P	Aam52113 Anthrax P	Aam51497 Anthrax P	Aam51496 Anthrax P		Aael8288 Bacillus	Aay56961 B. anthra		Aae18287 Bacillus		Aae18284 Bacillus	Aam50707 Bacillus	Aae07903 C. botuli	Aae07901 C. botuli	Aae07900 C. botuli	ပ	Aae35719 Clostridi	Aaw60224 Bacillus	Aays9277 MIS toxin	Aar91239 B. cereus
AAM51498	AAM52113	AAM51497	AAM51496	AAR60193	AAE18288	AAY56961	AAE18285	AAE18287	AAE18286	AAE18284	AAM50707	AAE07903	AAE07901	AAE07900	AAE07902	AAE35719	AAW60224	AAY59277	AAR91239
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26	27	28	50	30	31	32	33	3.4	35	36	3.7	80	6	40	41	42	43	4	45

ALIGNMENTS

	RESULT 1	T 1 604
	ID	AAM51494 standard; protein; 735 AA.
		AAM51494;
	ž È	01-RRB-2002 (first entry)
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.==.	-	Anthrax PA mutant K395D/K397D/D425K/D426K.
	X X	Anthrax; PA; profective antigen; antibacterial; pore-torming coxim; B mojetv: A-B anthrax foxin: Bacillus anthracis; vaccine; mutant; mutein.
_	SO	Bacillus anthracis.
		Synthetic.
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		/note= "Wild-type Asp substituted by Lys"
	NA S	WO200182788-AZ.
		08-NOV-2001.
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		WPI; 2002-017725/02.
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	PS	Claim 4; Page; 77pp; English.
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		-forming toxing (AAMS2113 and AAMS1484-AAMS1500), especially mutar
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Search completed: May 3, 2004, 19:39:59 Job time : 37.6261 8ec8

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1922 EDIIQERFSHNNI 106 -IRLEKGRLY-QI 1982 IIDIKNNETYPYI 164 RKKRSTSAGPTVP 2037 NKMKH		273 KNEDOSTONTDSE 	331 TVAIDHSLSLAGE : 2180 TI	379 PTTSLVLGKNQTI ::: : 2222 LINNVILNQNNM	435 NYNQFLELEKTKQLRLDT : : 2272 NNNYFDNWQLLNHNNLNN	477 WSEVLPQIQETTY ::: 2332 QNQI-PTI-ELDI	529 IAFGFNEPNGP 2388 ITNSLHNNNNNN	578 LDKIKLNAK :: 2448 LDKKEINVKNEE	633 KDIRKILSGYIVI : : : 2497 NNIDIISNGQNII	693 NYKVNVYAVTKENT : : 2551 NKSMNIEEGARKMKTNT	LT 15 OB1HP9 OB1HP9; O1.MAR-2003 (TERMBLrel. O1.MAR-2003 (TERMBLrel. O1.MAR-2003 (TERMBLrel. D1.MAR-2003 (TERMBLrel. D1.MAR-2003 (TERMBLrel. PF01 0480 PRID 0480 PRID 0480 RELEARYOTE Alveolata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 QEVINKASNSNK--------IRLEKGRLYQIKIQYQRENPTEKGLDFK-- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    680 IYIQNNHDQNNAPILQPINNHLAHINDLCYİHSEKNEYTKİSKNHÖMNNINPQQSNGKNQ 739
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5.2%; Score 197.5; DB 5; Length 2940;
st Local Similarity 18.7%; Pred. No. 0.94;
ches 162; Conservative 138; Mismatches 322; Indels 243; Gaps
Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., Mcradden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.; Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                   falciparum.";
Nature 419:498-511(2002).
BMBL; AE014843; AAN36060.1; -.
Hypothetical protein.
SEQUENCE 2940 AA; 348040 MW; BF8748DBAD5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIK---- 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 QKSSNSRKKRSTSAGPTVPDRDNDGIPDS-LEVEGYTVDVKNK----RTFLS----PWI 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 IGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPI- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---YNVLPTISLVLGKNQTLATIKAD--ENQLSQILAPNNYYPSKNLAPIALNAQKDFSS 429
                                                                                                                                                                                                                                                                 MEDLINE-22255705; PubMed=1236864;
Gardner M.J. Hall N., Fung E., White O., Berriman M., Hyman R.W.,
Gardner M.J., Hall N., Fung E., White O., Berriman M., Fyan A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
Eisen J.A., Rutherford K. Salzberg S.L., Craig A., Kyes S.,
Chan M.-S., Nehe V., Shallom S.J., Sub B., Peterson J., Angluoli S.,
Pertea M., Allen J., Selangut J., Haft D., Mather M.W., Vaidya A.B.,
Martin D.M.A., Pairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
McRadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
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                                                                                                                                                                                     Plasmodium falciparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE014825; AAN37143.1; -.
InterPro; IPR000008; C2.
Pfam; PF00168; C2; 5.
SMART; SM00239; C2 DOMAIN 2; 2.
PROSITE; PESD004; C2 DOMAIN 2; 2.
SEQUENCE 1904 AA; 224720 WW; AA36470367BDEC41 CRC64;
                                                                                                      QBIKS2;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
               Query Match 5.4%; Score 203.5; DB 5; Best Local Similarity 19.8%; Pred. No. 0.28; Matches 174; Conservative 129; Mismatches 327;
NDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS 717
                                                                                           PRT; 1904 AA
                                                                                          PRELIMINARY;
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                                                                                                                                                           Ferlin, putative.
PF14_0530.
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SEQUENCE FF
STRAIN=3D7;
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1483
SYNNIVL------QNDTRINIVRYNGYNDAMINAMINDAYKONIYNASQFGVINYNYYYD 1244
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Plasmodium falciparum (isolate 3D7).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBI_TaxID=36329;
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EMBL, AE014841, AAN35975.1; -.
Hypothetical protein. 335916 MW, B5515D173D96B813 CRC64;
SEQUENCE 2849 AA, 335916 MW,
                                                                                                                                                                                                                  ---GKDLNLVERRIAAVN-
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E.Y.,

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STRAIN-Serovar 3;
MEDLINR-20550219; PubMed=11048724;
Glass J.I., Lefkowitz E.J., Glass J.S., Cassell G.H.;
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                                         506F7D62999BA7B1 CRC64;
                                                                            Query Match 5.7%; Score 216.5; DB 5; Best Local Similarity 19.0%; Pred. No. 0.15; Matches 159; Conservative 130; Mismatches 275;
                     ll protein.
3468 AA; 411913 MW;
  EMBL; AE014841; AAN35955.1;
                   Hypothetical
SEQUENCE 34
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                                                                                                                                                                                                                                                                                78
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                                                                                                                                                                                                                                                                                LLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYT
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                                                                                                                                                                                                                                                                                                                                                                                   FATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTD
                                                                                                                                                                             Length 4688;
"The complete sequence of the mucosal pathogen Ureaplasma urealyticum.";
Nature 407:757-762(2000).
EMBL; ARF002145; ARF30894.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 4688 AA; 534880 MW; B53ABFAFFEB1997E CRC64;
                                                                                                                                                                                                                                Indels
                                                                                                                                                                             5.5%; Score 206; DB 16; Ilarity 21.3%; Pred. No. 0.68; Conservative 132; Mismatches 324;
                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 174; Conserv
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Q9PQ08; 01-OCT-2000 (TrEMBLrel, 15, 01-OCT-2000 (TrEMBLrel, 15, 01-MAR-2003 (TrEMBLrel, 23, Hypothetical protein UU482.

PRELIMINARY;

800d60

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955 KGLLYSTNNMKVDFKENFLNDKAELYSSG------DITIN-SENG-TFTNRVG 999
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                                                                                  SUNITSSUNIUMSKNIFVMGNIKISHNIANSGVIEGLELNTNSIENTGNITIKNKLTSQNL 603
                                                                                                                               STSRIHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSIVA---IDHSLSLAGERTWAETM 350
                                                                                                                                                 604 NNKK------NTANVNAGFLDVHNKISS-VGNIKAITMKINNLDNSGNIL-----TN 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                              576 TVLD----KIKLNAKMNILIRDKRFHYDRNNIAV-----GADESVVKBAHREVINSS--T 624
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                                                                                                                                                                                                                                                                                      ---IPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKV
                                                                                                                                                                                                351 GLNTAD-----TARINANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIKADENQLSQ
                                                                                                                                                                                                                                                               404 ILAPNNYYPSKALAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYN
                                                                                                                                                                                                                                                                                                                                464 FENGRVRVDTGSNWSEV-----LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE
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                   649 SLTTAENINKGSITAKNISNQNLVNSGS------DN
                                                                TGRIDKNVSPEARHPLVAAYPIVHVDMEN-----IILSKNEDQSTQNTDSETRIISKNT
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Janamodium Alloparum (isolate 3D7).
Bukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
NCBI_TaxID=36329;
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Nature 419:498-511(2002).
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Last sequence update)
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(TrEMBLrel. 23, I
(TrEMBLrel. 23, I
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     1 MESLGINNIYNALDRIKLNAKMNILVRDP-YHYDNNGNIVGVDDSYLKNAYKQILNWSSD 59
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Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Rapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhatteacharyva A., Bartman A., Gardner W., Grechkin G., Zhu L., A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Ingenome sequence and analysis of the ozal bacterium Fusobacterium nucleatum strain ATCC 25586.";

J. Bacteriol. 184:2005-2018(2002).

E. March A. Mandal ATCC 25586.";

J. Bacteriol. 184:2005-2018(2002).

R. GO; GO:0016020; Emembrane; IEA.

GO; GO:0016020; Emembrane; IEA.

R. GO; GO:0016020; Emembrane; IEA.

R. GO; GO:0016020; Emembrane; IEA.

R. GO; GO:0016020; Emembrane; IEA.

R. GO; GO:0016020; Emembrane; IEA.

R. InterPro; IPR008639; Haemagg act.

R. InterPro; IPR008639; Peptidase_S26.

R. InterPro; IPR004529; SH3.

R. InterPro; IPR004529; SH3.
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                                      ---GLKEVINDRYDMLNISSLRQDG
                                                        673 KTFIDFKKYNDKLPLYISNPNYKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233; Gaps
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Fusobacterales; Fusobacteriaceae;
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20.8%; Pred. No. 0.043;
ive 131; Mismatches 303;
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                                        626 GLLLNIDKDIRKILSGYIVEIEDTE----
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Pfam; PF00018; SH3; 1.
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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Bacteria; Fusobacteria;
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Matches 175; Conserv
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SEQUENCE 1881 A
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NCBI_TaxID=76856;
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                                                                                                                                     367 VGSD--WGNSKSNTEQFNSASAGYLNANVHYNNVGTGGIYDAQPTTSFIL-QDSTIATIT 423
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                                                                                                                                                                                  340 LAGERTW----AETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIK 395
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                                                                                                         283 DSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS
216 QKMKRDIDED---TDTDGDSIPDLWEENGYT--IQNK--VAVKW-DDKFAQQGYVKYLSS
                                                        SSTEGLL----LNIDKDIRK----ILSGYIVE--IEDTEGLKEVI---NDR
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MEDLINE=22061436; PubMed=12004073;
MEDLINE=22061436; PubMed=12004073;
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Read T.D., Salzberg S.L., Read T.D., Schupp J.M., Solomon D.,
Keim P., Fraser C.M.;
"Comparative Genome Sequencing for Discovery of Novel Polymorphisms Bacillus anthracis.";
Science 295:2028-2031(2002).
BMBL, AE011190; AAM26108.1; -.
BMBL, AE011140; AAM26108.1; -.
Plasmid.
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NCBL_TaxID=1392;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 7.9%; Score 296.5; DB 2; Local Similarity 37.2%; Pred. No. 6.9e-07; nes 68; Conservative 38; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225
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01-OCT-2002 (TEMBLES 22,
01-OCT-2002 (TEMBLES 22,
01-JUN-2003 (TEMBLES 24,
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Bacillus anthracis.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121
                                                                                                   287 TKSMSKSTSHSSTNINTV--GAEVSGSLQLAGGIFPVFSMSASANYSHTWQNTSTVDDT- 343
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                           SVSAGFSNSNSSTVAIDHSL 338
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"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";
"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";
"Cloning of Vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";
BMB., AY24547, AA086514.1;
GO; GO:0015576; C:extracellular; IEA.
GO; GO:0015076; F:toxin activity; IEA.
GO; GO:00150405; P:pathogenesis; IEA.
InterPro; IPR003696; Anthrax toxinB.
Pfam; PF03495; Bliant toxinB.
PRINTS; PR01391; BINARYTOXIB.
SEQUENCE 775 AA; 87110 MW; 416B25394361B731 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 QENRILLNESESSSQGILGYYFSDINFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RENPIEKGLD-----PKLYWTDSQNKKEVISSDNLQLPELKOKSSN------
                                                                                                                                                                        344 --TGE-SFSQGLSINTGBSAXINPNIRYYNTGTAPVYNVTPTTTIVIDK-QSVATIKGQB
                                                                                                                                                                                                                           399 NOLSOILAPNNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGN
                                                                                                                                                                                                                                                  460 FAXXN-SNGNLVTD-GNNWGPYLGTIXSTTASLTLSFSGQTTQVA----VVAPNFSDPEDK
                                                                                                                                                    339 SLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADE
                                                                                                                                                                                                                                                                                                 459 IATYNFENGRVRVDTGSNWSEVLPQIQETTARII--FNGKDLNLVERRIAAVNPSDPLET
                                                                                                                                                                                                                                                                                                                                                                        TKPDMTLKEALKIAFGFNEPNGNLQYQGKDIT----BFDFNFDQQTSQNIKNQLAELNATN
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19.3%; Score 728; DB 2; Length 775;
Best Local Similarity 29.1%; Pred. No. 1.3e-26;
Matches 224; Conservative 133; Mismatches 293; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacillus thuringiensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1428;
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Last sequence update)
Last annotation update)
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                                                                                TRTISKNTSTSRTHTSEVHGNAEVHASFFDIGG
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SNAKLKANANRDTDRDGIPDEWEINGYTVMNQKAVAWDDKFAAN-----GYKKYVSNPFK 230
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586 IIKEQLKYLDDKKIYNV----KLERGMNILIKVPSYFTNFDEYNNFP--ASWSNIDTKNQ 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. SYCHANDE OF C. S. SEQUENCE. C. X. MEDLINE=96184657; PubMed=8645309; Kimura K., Ohishi I., Moriishi K., A. Fuji N., Kubota T., Shirakawa S., Kimura K., Ohishi I., Moriishi K., I Isogai E., Isogai H.; Shirakawa S., Kimura K., Ohishi I., Moriishi K., I Isogai E., Isogai H.; Somponent-I gene of botulinum C2 toxin and PCR RT detection of its gene in clostridial species."; RI Biochem. Biophys. Res. Commun. 220:353-359(1996).

BR. Biochem. Biophys. Res. Commun. 220:353-359(1996).

BR. Biochem. Biophys. Res. Commun. 220:353-359(1996).

BR. C. SELIZAZI IACC. C: Extracellular; IEA.

BR. GO; GO:0005405; C: Extracellular; IEA.

BR. GO; GO:0009405; P:pathogenesis; IEA.

BR. GO; GO:0009405; P:pathogenesis; IEA.

BR. InterPro; IPR003896; Anthrax toxinB.

BR. InterPro; IPR003896; Anthrax toxinB.

BR. PFM, PF03495; Binary toxB; I.

BR. PRIMTS; PR01391; BINARRYTOXINE.

SQ. SEQUENCE 721 AA; 80515 MW; 44C8153AC749D5F2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 KQENRILINESES -- SSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                   700 EKDYTKFŠYEFETTGKDSSDIEITLTSSGVIFLDNLSITELNSTPEILKEPEIKVPSDQE
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                                                                                       640 DGLQSVANKLSGETKIIIPMSKLKPYKRYVPSGYSKDPSTSNSITVNIKSKEQKTDYLVP
                                                618 EVINSSTEGL -----LLINIDKDIRKILSGY -----IVEIEDTEGLKEVIND
                                                                                                                                          ---SLRQDGKTFIDFKKYND--KLPLYISNPNYKV----
                                                                                                                                                                                                                                                                                                                                                                                                                             086171;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-2003 (TrEMBLrel. 24, Last annotation update)
C2 toxin (Component-II).
C1 strindium boculinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=type C;
MEDLINE=98323874; PubMed=9659689;
Mimura K., Kubota T., Ohishi I., Isogai H., Isogai E.,
The gene for component-II of botulinum C2 toxin.";
Vet. Microbiol. 62:27-34(1998).
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YOREN------PTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PFIPNNNFFDVRFFSAAWEDEDLDTDNDNIPDAYEKNGYTI----KDSIAVKWNDSFA 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VAIDHS------LSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSL 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 AGPTVP--------DRDNDGIPDSLEVEGYTVDVKATFLSPWISNIH 211
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                                                        STRAIN=NCIB 10748;
MEDLINE=94041637; PubMed=8225592;
Perelle S., Gibert M., Boquet P., Popoff M.R.;
"Characterization of Clostridium perfringens iota toxin genes and expression in Bscherichia coli.";
Infect. Immun. 61:5147-5156(1993).
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Local Similarity 31.2%; Pred. No. 1.5e-33;
tes 253; Conservative 130; Mismatches 278; Indels 150;
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STRAIN-MCIB 10748;
Popole F. M.R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X73562; CAA31960.1; -.
ETR.; 140862; 140862.
HSSP; P13423; 1ACC.
R GO; GO:0005576; Cextracellular; IEA.
GO; GO:0015070; F:toxin activity; IEA.
GO; GO:0015070; F:toxin activity; IEA.
R GO; GO:0015070; F:toxin activity; IEA.
R GO; GO:0015070; B:toxin activity; IEA.
R FRAN; PR03495; B:DIARY toxB; 1.
R PRINTS; PR01391; BINARYTOXINB.
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875 IOTA TOXIN COMPONENT IB,
98468 MW; C9AE092CD3818921 CRC64;
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                                                              LSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAD 397
----DQGKTVSRNTINSKTDANTAGVAINIAYQNGF---TGSITTNYSHTTENSTAVQNS 373
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SEQUENCE FROM N.A.

STRAIN-CCUG 20309;
Carang S.Y., Song K.P.;
Range-ribosylating Binary Toxin Genes of Clostridium difficile strain "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain "ADP-ribosylating Binary Toxin Genes of Clostofologon";
CCUG 20309.";
REMBL; AF711719; AAF81761.1; -.
RHSSP; P13423; 1ACC.
R GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; P:pathogenesis; IEA.
R GO; GO:0009405; P:pathogenesis; IEA.
R GO; GO:001391; Binary_toxinB.
Pfam; PF03495; Binary_toxinB.
R PRINTS; PR01391; Binary_toxinB.
S PRINTS; PR01391; Binary_toxinB.
S PRINTS; PR01391; Binary_toxinB.
S PRINTS; PR01391; Binary_toxinB.
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                                                                    KKKEIVNEDILPNNGLMGYYFTDEHFKDLKIMAPIKDGNLKFEEKKVDKLLDKDKSDVKS
                                                                                                     AIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR
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                                                      4 QENRILINESESSSQGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN-IPSENQYFQS
                                Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
10ta toxin component Ib precursor.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1502;
                                125;
         Length 876;
                                Indels
23.3%; Score 880.5; DB 2;
31.6%; Pred. No. 9e-34;
Micmatches 280;
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                   larity 31.6%; Pred. No. 9e-34
Conservative 139; Mismatches
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                     Similarity
                       Best Local Simi
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                                                                                                                                                                                                      ETKIKIPMSELKPYKRYVFSGYSKDPLTSNSIIVKIKAKEEKTDYLVPEQGYTKFSVEFE
       NIYTVLDKIKLNAKANILIRDKRFHY---DRNNIAVGADESVVKEAHREVINSSTEGL--
                                                                               599 KIYNV----KLERGMNILIKTPTYFTNFDDYNNYP--STWSNVNTTNQDGLQGSANKLNG
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Last annotation update)
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Bacteria; Firmicutes; Mollicutes.
NCBI_TaxID=29348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR
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EMBL, 176081, AAB67305.1; -188P; P13422; IACC.
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                              05, Created)
05, Last sequence update)
24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 23.4%; Score 882.5; DB 2; Best Local Similarity 31.7%; Pred. No. 7.3e-34; Matches 252; Conservative 138; Mismatches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; IEA.
GO; GO:001570; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IFR003896; Anthrax toxinB.
Pfam; PF03495; Binary toxB; 1.
PRINTS; PR01391; BINARYTOXINB.
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                                                                                                                                     ADP-ribosyltransferase
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Bacteria, Firmicutes;
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                                                                                                                                                                                                                                                                                      Clostridium.
NCBI_TaxID=1496;
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97.7%; Score 3689; DB 2;
Best Local Similarity 99.4%; Pred. No. 7.8e-167;
Matches 718; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                     292757AD2D5DE5A6
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EMBL; AJ413936; CAC93934.1; -. GO, GO:0005576; C:extraccllular; IEA. GO; GO:0004521; C:extraccllular; IEA. GO; GO:0015070; F:toxin activity; IEA. GO; GO:0009405; P:pathogenesis; IEA. InterPro; IPR03396; Anthrax toxinB. PRINTS; PR03495; Binary_toxB; I. PRINTS; PR03495; Binary_toxB; I. PRINTS; PR03495; Althrax toxinB. Pafamid.

NON_TER 1

NON_TER 743 743

SEQÜENCE 743 AA; 83363 MW; 292757AD2D5D
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                                                                                                     ORENPTEKGLDFKLYWTDSONKKEVISSDNLOLPELKOKSSNSRKKRSTSAGPTVPDRDN
           QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Adone R., Pasquali P., La Rosa G., Marianelli C., Muscillo M.,
Fasanella A., Francia M., Ciuchini F.;
Sequence analysis of the genes encoding for the major virulence
factors of bacillus Anthracis vaccine strain 'Carbosap'.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Bacillus anthracis.
Plasmid pXO1.
Bacteria, Firmicutes; B
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sp_unclassified:*
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ALIGNMENTS

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AC C037W2

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TO 1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

TO 1-UUN-2003 (TrEMBLrel. 19, Last sequence update)

DE Pag protein (Fragment).

Bactlius anthracis.

OG Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

ON NORI TAXID=1392;

RN SEQUENCE FROM N.A.

RA Adone R., Francia M., Ciuchini F.;

RA Adone R., Francia M., Ciuchini F.;

RA Adone R. Pasanella A., Francia M., Ciuchini F.;

RA Fasanella A., Francia M., Ciuchini F.;

RA Adone R. Sequence analysis of the genes derain (Carbosap.";

RA Adone R. Francia M. Ciuchini F.;

RA Adone R. Sequence analysis of the genes derain (Carbosap.";

RA Bach Last Sequence analysis of the major virulence R. Submitted (SED-2001) to the EMBL/GenBank/DDBJ databases.

BR Co.; OG:0005576; C:extrachromosomal DNA; IEA.

DR GO; GO:0005576; C:extrachromosomal DNA; IEA.

DR GO; GO:0005576; C:extrachromosomal DNA; IEA.

DR GO; GO:0005676; P:extrachromosomal DNA; IEA.

DR GO; GO:0005676; P:extrachromosomal DNA; IEA.

DR GO; GO:0005676; P:extrachromosomal DNA; IEA.

DR GO; GO:000576; P:extrachromosomal DNA; IEA.

DR FAINTS; PRO1399; Anthrax toxin B.

R FINTS; PR01391; BINARYTOXINB.

FT NON TER 741 A4; 93153 MW; C7F95820B73065C0 CRC64;

BOST Local Similarity 99.44; Pred. No. 78e-167;

BOST Local Similarity 99.44; Pred. No. 78e-167;

BOST Local Similarity 99.44; Pred. No. 78e-167;

BACCHOS 718; CORDS 718; PROSECUENCE 718; CORDS 718; Ratches 718; CORDS 718; Prod. No. 78e-167;
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1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60

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AAM51491 standard; protein; 735 AA.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AAM52113	AAM51498	AAM51496	AAM51497	AAR60193	AAE18288	AAY56961	AAE18285	AAE18287	AAE18286	AAE18284	AAM50707	AAE07903	AAE07901	AAE07900	AAE07902	AAE35719	AAW60224	AAX59277	AAR91239
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ALIGNMENTS

Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein. Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus /note= "Wild-type Asp substituted by Lys" Location/Qualifiers 04-MAY-2001; 2001WO-US014372. Claim 4; Page; 77pp; English. 04-MAY-2000; 2000US-0201800P. (first entry) Collier RJ, Sellman BR; Anthrax PA mutant D425K. (HARD) HARVARD COLLEGE. WPI; 2002-017725/02. Key Misc-difference 425 Bacillus anthracis. WO200182788-A2 01-FEB-2002 08-NOV-2001 anthracis. Synthetic

The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM51804-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                               /note= "Wild-type Asp substituted
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Pred. No. 1.3e-244;
1; Mismatches 0;
Location/Qualifiers
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Best Local Similarity 99.9%;
Matches 734; Conservative 1
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                                                                                                                                                                                                                                                                                                            thrax; PA; protective antigen; antibacterial; pore-forming toxin; moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
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                                                                                        DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                                                                                                                DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
             LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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                       Indels
 3; DB 5;
1.5e-244;
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 Score 3768;
Pred. No. 1.
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The invention relates to antibacterial agents comprising mutant forms of poer-forming toxins (AAMS12113 and AAMS1484AAM1500), especially mitants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. The present sequence is that of the anthrax PA protein
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Pred. No. 1.7e-244;
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killing tumour cells
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Pred. No. 1.7e-244;
0; Mismatches 1;
                                                                                                                                                                                                                                                                    Nucleic acid encoding anthrax toxin fusion targetting toxin to specific cells, eg for infected cells.
                                                                                                                                                                                      Arora N, Singh Y,
                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 81-83; 124pp; English.
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ilarity 99.9%;
Conservative
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25-JUN-1993;
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Local S...
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                                                                                                                                                     GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNBDQSTQNTDSETRTISKNTSTSRTHT
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QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSKKRSTSAGPTVPDRDN
                                                                                   DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                    DGI PDSLEVEGYTVDVKNKRTFLSPWI SNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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Misc-difference 425
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Synthetic.
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS213 and AAMS120), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                                                                                       Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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Pred. No. 1.7e-244;
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QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                                                                                                                    DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                               301 SEVHONAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL
                                                                                                                                                                                                                                           SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
                                                                                                                                                                                                                                                                                                                                                                                                                          LPQIQETTARIIFNGKDINLVERRIAAVNPSDPLBTTKPDMTLKRALKTAFGFNEPNGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>OYQGKDİTEFDFNFDQQTSQNIXNQLABLNATNIYTVLDXIKLNAKMNILIRDKRFHYDR</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 NNIAVGADESVVKEAHREVINSSTEGLLENIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                                                                                                                    GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                                                                                                                                                            361 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA
                                                                                                                                                                                                                                                                                                                                        LNAQKDFSSTP1TMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV
                                                                                                                                                                                                                                                                                                                                                          481 LPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
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                                                  241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 QYQGXDITBFDFNFDQQTSQNIKNQLABLNATNIYTVLDXIKLNAKMNILIRDKRFHYDR
                                ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                         DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; protective antigen; PA; MAT-PA; TPA-PA; activator; PA63; vaccine; anthrax; antibacterial
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tissue plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus anthracis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1464-AAMS150), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                        720
                                                    720
                                                                                                                                                                                                                                                                                                                Anthrax, PA, protective antigen, antibacterial; pore-forming toxin;
B moiety, A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
                                            DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                        DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      substituted
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Pred. No. 1.7e-244;
); Mismatches 1;
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397
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                                                                                                                                                                                                                                                                                    Anthrax PA mutant K397D/D425K.
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                                                                                                                721 IKKILIFSKKGYEIG 735
                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                      (first entry)
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nes 734; Conservative
                                                                                     IKKILIFSKKGYEIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 425
                                                                                                                                                                                             standard;
                                                                                                                                                                                                                                                                                                                                                              Bacillus anthracis.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 735 AA;
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Matches
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The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus anthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced from protective activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthrax or B. anthracis proteins. The present sequence represents a B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant DNA construct useful as vaccines for anthrax, in producing host cells for analyzing the drugs and agents inhibiting anthrax.
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DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; protective antigen; PA; MAT-PA; TPA-PA; activator; PA63; vaccine; anthrax; antibacterial.
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Pred. No. 1.8e-244;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 32, 35pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                           721 IKKILIFSKKGYEIG
                                                                                                                                                 722 IKKILIFSKKGYEIG
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N-PSDB; AAZ56876.
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tissue plasminogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Best Local Simil
Matches 734; C
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                                                                                                                                                                                                                                                        The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillue anthracis proteins, selected from protective antigen (PA). MAY-PA (PA with its secretory signals replaced with those of tissue plasminogen with its secretory signals replaced with those of tissue plasminogen activator) and PAS3 (63 MDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthracis MAT-PA proteins. The present sequence represents a B. anthracis proteins.
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                                                                                                                         binant DNA construct useful as vaccines for anthrax, in producing cells for analyzing the drugs and agents inhibiting anthrax.
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Pred. No. 1.7e-244;
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                                                                                                                                                                                                              Disclosure, Page 34; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 734; Conservative (
                                       2000-182165/16
                                                                     N-PSDB; AAZ56875.
                                                                                                                         Recombinant DNA
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568 540 0.09 628 660 689 DMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG 720 748 420 448 480 508 240 300 360 388 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL <u>OYĞĞKDİTEFDFNFDQQTSQNİKNQLAELNATNIYTVLDKİKLNAKMAILIRDKRFHYDR</u> DMLNI SSLRODGKTFI DFKKYNDKLPLYI SNPNYKVNVYAVTKENTI I NPSENGDISTNG GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL NANIRYVNIGTAPIYNVLPTISLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY IKKILIFSKKGYEIG 735 449 509 569 629 199 721 749 389 481 601 689 541 181 209 241 269 301 361 421 g ò d d g δ g $\overset{\sim}{\circ}$ 임 ò δ q δ g ò g 8 d ò

AAYS6958 standard; protein; 764 entry) (first 25-APR-2000 AAY56958

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Bacillus anthracis protein; protective antigen, PA; MAT-PA; TPA-PA; tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial B. anthracis protective antigen (PA) protein.

99WO-US015568 Bacillus anthracis WO200002522-A2 09-JUL-1999; 20-JAN-2000

Welkos ĢF, US MEDICAL RES INST INFECTIOUS Smith Pushko P, Parker MD, (USME-) Lee JS,

98US-0092416P

10-JUL-1998;

SL;

WPI; 2000-182165/16 N-PSDB; AAZ56874.

producing vaccines for anthrax, in Recombinant DNA construct useful as

IKKILIFSKKGYEIG 735

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629 420 480 509 540 569 600 099 689 720 749 300 329 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360 The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus anthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced with those of tissue plasminogen with its secretory signals replaced with those of tissue plasminogen activator) and PAS (63 MDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as weachnee for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthrax. Pure analyzing the effectiveness of drugs and agents that inhibit anthrax. 120 149 180 240 269 209 **8**0 OYQGKDITEFDENFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKONILIRDKRRFHYDR LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LNAQDDFSSTPITWNYNQFLELEKTKQLKLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 510 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMINISSIRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKBNQLSQILAPNNYYPSKNLAPIA ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVXNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT 1 EVKQENRLLINESESSSOGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF cells for analyzing the drugs and agents inhibiting anthrax ö Length 764; Indels Query Match
Best Local Similarity 99.9%; Pred. No. 1.8e-244;
Matches 734; Conservative 0; Mismatches 1; Disclosure; Page 33; 35pp; English anthracis PA protein Sequence 764 AA; 270 330 450 541 570 601 661 361 390 421 481 210 241 30 61 90 121 150 181 301 host ò g qq 8 B 8 g d ö ò D. ठ हे ठ g δ g à g $\dot{\delta}$ 염장 ઠે

89

EVKQENRLLNESESSSQGLLGYYFSDLNFQAPWVVTSSTTGDLSIPSSELENIPSENQYF

30

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LF4; protective antigen; PA; DNA vaccine;
                                                                                                                                                                                                                                                                                                                                                                   Protecting animal against lethal infection with Bacillus anthracis, by administering wildtype or mutated form of Bacillus anthracis lethal factor protein or its fragment or a nucleic acid encoding the mutated
                                                                                                                                        1..29
/label= Signal peptide
/label= Not given in the specification"
30..764
/label= PA
204..764
/label= pCPA
                                                                                       Lethal factor; LF; immunogen; LF4; protective a
humoral; cell-mediated; immune memory response.
                                                                     Wild type B. anthracis protective antigen.
                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                     (OHIS ) UNIV OHIO STATE RES FOUND.
(GALL/) GALLOWAY D R.
(MATE/) MATECZUN A J.
                 764
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                      99US-0171459P.
                                                                                                                                                                                                                                                     21-DEC-2000; 2000WO-US034912.
                AAB47306 standard; protein;
                                                                                                                                                                                                                                                                                                                        Galloway DR, Mateczun AJ;
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                           WPI; 2001-408540/43.
N-PSDB; AAC86016.
                                                                                                                Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 764 AA;
                                                                                                                                                                                                                 WO200145639-A2
                                                                                                                                                                                                                                                                      22-DEC-1999;
                                                    29-AUG-2001
                                                                                                                                                                                                                                  28-JJN-2001
                                   AAB47306;
                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                      Protein
                                                                                                                                                                                       Peptide
RESULT 11
         AAB47306
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This sequence shows the B. anthracis protective antigen (PA). An immunogenic fragment of PA, pCPA, can be used to produce an immune response which protects an animal against lethal injection with Bacillus anthracis. DNA encoding the B. anthracis PA can be used in conjunction with DNA encoding the B. anthracis PA can be used in conjunction with DNA encoding the mutated LF protein or fragment alone or in combination with a DNA encoding the PA protein or its fragment, both components (humoral and cell-mediated) of the immune system are stimulated, which results in longer term immune memory response. The combined use of a mutated LF and PA gene or their fragments results in a higher level of immune response, as judged by overall serum antibody titers for LF and PA antigens, than the use of either LF or PA genes in separate immunizations
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EVKOENRLLNESESSSOGLLGYYFSDLNFOAPMVVTSSTTGDLSIPSSELENIPSENQYF . 0 Query Match 99.8%; Score 3767; DB 4; Length 764; Best Local Similarity 99.9%; Pred. No. 1.8e-244; Matches 734; Conservative 0; Mismatches 1; Indels (

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420 449 480 629 960 360 330 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 389 509 540 569 600 689 720 749 240 269 300 149 180 209 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISING 541 ÇYÇGKDITEFDENFDÇÇTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKANEDQSTQNTDSETRTISKATTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY IKKILIFSKKGYEIG 735 ikkilirskkgyzig 764 630 069 721 750 481 601 661 61 90 121 150 181 210 241 270 301 361 421 8 & qq 엄 ò g ò g ò g ठ 음 6 엄 ò g ò ઠ 원 상 원 ð 8 ò

Antibacterial; Vaccine; immune response; Bacillus anthracis. Ź ADE65872 standard; protein; 857 Bacillus anthracis PA antigen. (first entry) Bacillus anthracis. WO2003087378-A1. 29~JAN-2004 ADE65872; RESULT 12 ADE65872

11-APR-2003; 2003WO-GB001553 23-OCT-2003.

11-APR-2002; 2002US-0371416P

ö 540 600 OYOGKDITERDENPDOQTSONIKNOLABLNATNIYTVLDKIKLNAKNNILIRDKRFHYDR 681 999 741 720 The present invention relates to a new polynucleotide vaccine composition comprising a nucleic acid sequence that encodes a Bacillus anthracis antigen and that is operatively linked to a promoter suitable for expression of the antigen in a mammalian cell. The polynucleotide vaccine composition is useful for eliciting a protective immune response against Bacillus anthracis. The present sequence represents Bacillus anthracis PA 240 300 360 441 420 501 480 561 621 120 180 261 321 381 141 201 seguence 60 DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG 202 GRENPTEKGLDFKLYMTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTRTHT GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQ1LAPNNYYPSKNLAPIA NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 562 LPQIQETTARIIFNGKDLNLVBRRIAAVNPSDPLSTTKPDMTLKBALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDPEKVT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL BVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIFSSELENIPSENQYF EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY Gaps New polynucleotide vaccine composition comprising a nucleic acid s that encodes a Bacillus anthracis antigen, useful for eliciting a protective immune response against Bacillus anthracis. . 0 Length 857; Indels 99.8%; Score 3767; DB 7; llarity 99.9%; Pred. No. 2.2e-244; Conservative 0; Mismatches 1; Example 1; SEQ ID NO 4; 65pp; English Fuller J; POWDERJECT RES WPI; 2003-877105/81. N-PSDB; ADE65871. Similarity Sequence 857 AA; Schmaljohn C, Query Match Best Local Simil Matches 734; (622 262 442 502 481 541 601 121 322 301 382 361 421 Н 82 142 181 241 61 ò 셤 à g ò ò q 임 δ qq ò 엄 δ g QQ $\stackrel{>}{\circ}$ 8 ò ď ò

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The present invention relates to an immunogenic reagent, which produces an immune response that is protective against Bacillus anthracis. The reagent comprises one or more polypeptides which together represent up to three domains of the full length Protective Antigen (PA) of Bacillus anthracis or variants of these, and at least one of the domains comprises domain or domain 4 of PA or its variant. The invention is used as a vaccine. The immunogenic reagent is useful in the preparation of a medicament for the prophylaxis or treatment of B. anthracis infection. The present sequence is Bacillus subtilis protective antigen domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVKQENRLLNESESSSQGLLGYYPSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic reagent having a polypeptide of the full length Protective Antigen of Bacillus anthracis, useful for treating B. anthracis infection or in preparing a medicament for the prophylaxis treatment of the infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holden PT;
AW;
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0
                                                                                                                                                                                                            PA;
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                                                                                                                                                                                                         Immunogenic reagent; immune response; protective antigen;
Bacillus anthracis infection; antibacterial.
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                                                                                                                                                                                domain 1+2+3+4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller J, Walker NJ, Baillie LWJ,
Bullifent HL, Titball RW, Topping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 3764; DB 5; 99.7%; Pred. No. 2.8e-244; iive 1; Mismatches 1;
                                                                                                                                                                                  (PA)
                                                                                                                                                                                                                                                                                                         /note= "Encoded by GAA"
                                                                                                                                                                                  Bacillus subtilis protective antigen
                                                                                                                                                                                                                                                                               Key Location/Qualifiers Misc-difference 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 3; 40pp; English.
                                                                                                  735
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                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUL-2000; 2000GB-00016702,
                                                                                                    standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (MINA ) UK SEC FOR DEFENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.7'
Matches 733; Conservative
                                                                                                                                                         (first entry)
     IKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-171720/22.
N-PSDB; AAD29121.
                                                                                                                                                                                                                                                       Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 735 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williamson ED,
Flick-Smith HC,
                                                                                                                                                                                                                                                                                                                                        WO200204646-A1
                                                                                                                                                         07-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2002
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                                                                                                                             AAE18289;
       721
                                                                                                    AAE18289
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DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG

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540 360 420 420 480 480 540 600 600 9 999 720 180 240 300 300 Apoptosis; therapy; inflammatory mediator; intracellular trafficking; infection; Prion disease; Alzheimer disease; hypersecretion disorder; muscle spasm; COPD; bronchitis; chronic obstructive pulmonary disease; torticolis; blephorospasm; asthma; protective antigen. DMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG DMLNISSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSQTRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL QYQGKDITEFDFWFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLILNIDKOIRKILSGYIVEIEDTEGLKEVINDRY QRENPTEKGL, DFKL, YWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGIPDSLEVEGYTVDVKNKKTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNIGTAPIYNVLPITSLVLGKNOTLATIKAKENOLSOILAPNNYYPSKNLAPIA NANIRYVNIGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIPNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIARGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY antigen (MICR-) MICROBIOLOGICAL RES AUTHORITY Ā standard; protein; 764 Bacillus anthracis protective 735 21-MAY-2002; 2002WO-GB002384 24-MAY-2001; 2001GB-00012687 (first entry) IKKILIFSKKGYEIG IKKILIFSKKGYEIG WO200296467-A2. 17-JUN-2003 AAE35717; Bacillus 601 661 199 721 721 301 361 421 481 481 541 601 AAE35717 361 421 121 181 181 241 301 RESULT 14 AAE35717 엄 ò 임 ò Db ò 임 ò Db В δ g 8 S B Ωp δ 8 8

The invention relates to a conjugate comprising an injected bacterial effector protein and a carrier that targets the effector protein to a carge cell. Pharmacutical composition of the invention is useful for a create cell. Pharmacutical composition of the invention is useful for a treatment selected from promocing or inhibiting survival of cells, promocing or inhibiting the growth of cells, apoptosis, release of an inflammatory complicator from cells, division of cells and treating intracellular complicator from cells, division of cells and treating intracellular cell useful in the manufacture of a medicament for treating a neuronal cell, for intracellular infection, for interfering with intracellular cell, for intracellular cell. The invention is also useful for inhibiting secretion from cells. The invention is also useful for treating Prion disease, Alzhaner disease and wide range of disorders including muscle spasms such as blephorospasm, torticols and disease (CODP), bronchitis and ashman. The present sequence is Bacillus anthracis continuantion of the invention ô 509 540 360 SEVHÇINAEVHASPFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADTARL 389 420 449 480 569 120 149 180 209 240 269 300 329 Conjugate for modulating cell survival and cell growth, modulating release of inflammatory mediator from cells, comprises injected bacterial effector protein and a carrier that targets the protein to target cell. 9 89 LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGI PDSLEVEGYTVDVKAKRTFLSPWI SNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF EVKQENRLINESESSSQGLIGYYFSDLNFQAPWVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN DGI PDSLEVEGYTVDVKAKRTFLSPMI SNIHEKKGLTKYKSSPEKWSTASDPYSDPEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT NANI RYVNTGTAPI YNVLPTTSLVLGKNOTLATI KAKENOLSOILAPNNYYPSKNLAPIA Gaps ö Length 764; Indels Score 3764; DB 6; Pred. No. 2.9e-244; 1; Mismatches 1; Example 12; Page 122-125; 130pp; English Query Match
Best Local Similarity 99.7%;
Matches 733; Conservative 1 Sequence 764 AA; invention 150 210 270 390 450 510 \dashv 30 61 0 181 301 330 361 421 481 121 241 d à 8 8 g ઠ g ⋧ qq 8 g ઠે 셤 ઠ g ò à

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Shone

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Sutton

WPI; 2003-167247/16

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OYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKONILIRDKRFHYDR

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us-09-848-909a-8.rag

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1484-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (FA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
                                                        689
                                                                                    720
                             099
629
                                                                                                     DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 749
                                                                                                                                                                                                                                                                                                                                                                  Anthrax, PA, protective antigen, antibacterial, pore-forming toxin, B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant, mutein.
                                             NNIAVGADESVVKEAHREVINSSTEGLILMIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                             NNIAVGADESVVKRAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                                                     DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3763; DB 5; Length 735;
Pred. No. 3.2e-244;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Wild-type Lys substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key Location/Qualifiers
Misc-difference 397
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                                                                                                                                                                                                                                                AAM51487 standard; protein; 735
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Best Local Similarity 99.7%;
Matches 733; Conservative
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                                                                                                                                            IKKILIFSKKGYEIG 735
                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                        Anthrax PA mutant K397Q.
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                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus anthracis.
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                                         QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSKKKRSTSAGPTVPDRDN
                                                                      DGI PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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                            ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model	Run on: May 3, 2004, 19:31:43 ; Search time 15.0966 Seconds (without alignments) 2513.152 Million cell updates/sec	Title: US-09-848-909A-8 Perfect score: 3773 Sequence: 1 EVKQENRLINBSESSSQGLLTSTNGIKKILIFSKKGYEIG 735	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 389414 seqs, 51625971 residues	Total number of hits satisfying chosen parameters: 389414	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : Issued Patents AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:* 6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	3767 99.8 735 1 US-08-021-601-4 Sequence 4, 3767 99.8 735 1 US-08-082-849B-4 Sequence 4,	3722.5 98.7 903 1 US-08-021-601-12 Sequence 12	3/22.5 98.7 903 1 US-08-082-8495-12 Sequence 12 3722.5 98.7 903 5 PCT-US94-01624-12 Sequence 12 Sequence 12	3590 95.1 719 5 PCT-U894-01624-31 Sequence 31	9 12/3 33.6 288 4 US-US-12/3-839A-8 Sequence 0. 0 781 20.7 881 3 US-08-960-780-32 Sequence 32	2 781 20.7 881 4 US-09-307-106-8 Sequence 32 781 20.7 881 4 US-09-850-351A-32 Sequence 3.2	4 779 20.6 884 1 US-08-471-033-5 Sequence 5, 5 779 20.6 884 2 US-08-471-044-5 Sequence 5,	6 779 20.6 884 2 US-08-463-483A-5 Sequence 5, 779 20.6 884 2 US-08-471-046A-5 Sequence 5, 203-08-471-046A-5 Sequence 5, 203-08-20-20-20-20-20-20-20-20-20-20-20-20-20-	8 779 20.6 884 2 US-08-470-566B-5 Sequence 5, 9 779 20.6 884 2 US-08-469-334-5 Sequence 5, 0 779 20.6 884 3 US-09-300-529-5 Sequence 5,	21 779 20.6 1346 1 US-08-471-033-23 Sequence 23, Appl 22 779 20.6 1346 2 US-08-471-0423 Sequence 23, Appl 23 779 20.6 1346 2 US-08-463-4833-23 Sequence 23, Appl	4 779 20.6 1346 2 US-08-471-046A-23 Sequence 23 5 779 20.6 1346 2 US-08-470-566B-23 Sequence 23	6 779 20.6 1346 2 US-08-469-334-23 Sequence 23 7 779 20.6 1346 3 US-09-300-529-23 Sequence 23

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US-08-082-849B-4
US-08-082-849B-4
Sequence 1, Application US/08082849B
Patent No. 5677274
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Yaven
APPLICANT: Singh, Yagendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: US-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber Kenneth A.
REGISTRATION NUMBER: 31,677
REGISTRATION NUMBER: 31,677
REGISTRATION NUMBER: 31,677
TELEFRAX: (415) 576-0200
TELEFRAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acida
TVPR: amino acida
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Pred. No. 1.3e-256;
0; Mismatches 1;
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llarity 99.9%;
Conservative
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TYPE: amino acida;
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-082-849B-4
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Best Local Similarity
Matches 734; Conservat
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481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540
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541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                                    SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
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Sequence 12, Application US/08021601
Fatent No. 591631
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Arora, Naveen
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESS:
ADDRESSEE: Navede & Rosenberg, P.C.
STREET: 133 Carnegie Way, Suite 400
COUNTRY: G. USA
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM DATA:

APPLICATION NUMBER: US/08/021,601

FILING DATE: 19930212

CLASSITEATION NUMBER: 34

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414.057

TELEPHONINICATION INFORMATION:

TELEPHONINICATION INFORMATION:

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                         DMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
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COMPERS PONDENCE ADDRESSS:
ADDRESSEE: TOWNSEND AND TOWNSEND KHOURIE and CREW
ADDRESSEE: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 4105
COMPUTER READABLE FORM:
NEDIUM TYPE: Floopy disk
COMPUTER: Datentin Release #1.0, Version #1.25
SOFTWARE: Parentin Release #1.0, Version #1.25
SOFTWARE: Parentin Release #1.0, Version #1.25
SOFTWARE: Parentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: Une 25, 1993
CLASSIFICATION NUMBER: 31,677
REPERAN: (415) 543-5043
INPORMATION POR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acids
TOPOLLOGY: linear
MOLECULE TYPE: protein
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99.8%; Score 3767; DB 5;
Best Local Similarity 99.9%; Pred. No. 1.3e-256;
Matches 734; Conservative 0; Mismatches 1;
                                                                             721 IKKILIFSKKGYEIG 735
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Pred. No. 2.3e-253;
1; Mismatches 3;
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Best Local Similarity 99.0%;
Matches 727; Conservative
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
TYPE: AMINO ACID
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                                       TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-021-601-12
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Sequence 12, Application US/08082849B; Patent No. 567224; GENERAL INFORMATION: APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen

RESULT 5 US-08-082-849B-12

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APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Related Methods
UNUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCES: 35
COUNTY: California
COUNTY: California
COUNTY: California
COUNTY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM-TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-005/MS-DCS
CORPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/08/082,849B
FILING DATE: 25-UNN-1993
CLASSIPPLICATION NUMBER: US/08/08/082,849B
FILING DATE: 25-UNN-1993
CLASSIPPLICATION NUMBER: US/08/08/082,849B
FILING DATE: 12-FEB-1993
ATTORNEY AGBNT INFORMATION:
MAME: Webber, Kenneth A.
REGISTRALION NUMBER: 15-2000
TELEFAM: (415) 576-0200
TELEFAM: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE: CARRACTERISTICS:
LENGTH: 903 anino acide
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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421	481	481	. 41 141		601		661	721	721	RESILL'T 6	94-01	GENERAL APPLI	APPLICANT:	APPLICANT	AFFLICANI TITLE OF	NUMBER OF	ADDRESS	STREET:	CITY:	5 E	ZIP: 9	COMPUTER READABLE MEDIUM TYPE: F.	COMPUTER:	SOFTWAR	APPLICA	FILING	ATTORNEY/ NAME:	REGISTR	TELECOMMU	TELEPHO	INFORMATION	LENGTH:	TYPE: am TOPOLOGY:) MOLECULE TY PCT-US94-01624-1	Query Match	Best Local S Matches 727	
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641 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKOMILIRDKRFHYDR 600
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1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60
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                                          QSAIWSGFIKVKKSDEYTPATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                   QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Patent No. 5677274
GENERAL INFORMATION:
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Nichols, Peter J.
TILLE OF INVENTION: Anthrax Toxin Fusion Proteins and TITLE OF INVENTION: Alited Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-384
KEDIUM TYPE: Floppy disk
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721 IKKILKKVVLGKKG 734
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                                      657 NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT
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                                                                                                                                                                                                                                                                     APPLICANT: Appla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen APPLICANT: Arora, Naveen APPLICANT: Arora, Naveen APPLICANT: Arora, Naveen APPLICANT: Nichols, Peter J. TILLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND TITLE OF INVENTION: ARLATED METHODS NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ACRRESPONDENCE ADDRESS: CRREST: Steuart Street Tower, 20th Floor, One Market STREET: Plaza CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A. REGISTRATION NUMBER: 31,677
REJECTRATION NUMBER: 31,677
REPERENCE/DOCKET NUMBER: 15280-115
TELECHONE: (415) 543-560
TELECHONE: (415) 543-560
TELECHONE: (415) 543-560
TELERAN: (415) 543-560
TELERAN: (415) 543-560
TELERAN: (415) 543-560
SURPRICE CHARACTERISTICS:
SURPRICE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 3590; DB 5;
Pred. No. 3.5e-244;
4; Mismatches 6;
                                                                                                                                                                                                                                    ; Sequence 31, Application PC/TUS9401624; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94105
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             735
                                                                                                                  717 STNGIKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.4%;
Matches 705; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 719 amino acids
amino acid
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PCT-US94-01624-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNTATIMMQRGNFLQGPTVP 180
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTUMEN: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-PBE-1993
ATTORNEY AGENT INFORMATION:
NAME: Weber, Kenneth A.
REFERENCE/DOCKET NUMBER: 15280-161-1
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARRETICS:
'TELEFER: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARRETICS:
'TEMPERATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 3590; DB 1;
Pred. No. 3.5e-244;
4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 95.4%;
Matches 705; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                      725
                                             209 SSLRQDGKTFIDFFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL 268
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APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Narva, Kenneth E.
APPLICANT: Schoelts, James
APPLICANT: Schoelts, James
APPLICANT: Schoelts, James
APPLICANT: Lower, David
APPLICANT: Lower, David
APPLICANT: Stamp, Lisa
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: No. 6204435el Pesticidal Toxins
NUMBER OF SEQUENCES: 134
CORRESPONDENCE ADRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 QENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                      SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
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ZIP: 3266-669

CONTRY: US

ZORPITER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/960,780

FILING DATE: 30-OCT-1997

CLASSIFICATION NUMBER: US 60/029,848

FILING DATE: 30-OCT-1996

APPLICATION NUMBER: US 60/029,848

FILING DATE: 30-OCT-1996

APPLICATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

REGISTRATION NUMBER: 31,794

RELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8800

TNFORMATION FOR SEC. 710 NO. 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 20.7%; Score 781; DB 3; I al Similarity 30.4%; Pred. No. 1.4e-46; 245; Conservative 134; Mismatches 298;
                                                                                                                                                                                                                                                                                Sequence 32, Application US/08960780 Patent No. 6204435
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US-08-960-780-32
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LENGTH: 881 amino acide
TYPE: amino acid
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                                                                                                                   726 IFSKKGYRIG 735
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Best Local Si
Matches 245;
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                                                                                                                                                                                                                                       361 TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNL 420
                                                                                                                                                                                                                                                                                     417 APIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN 476
                                                                                                                                                                                                                                                                                                                                                                               477 WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP 536
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Sequence 8, Application US/09273839A

Parter No. 63291E.

APPLICANT: Cirino, Nick M

APPLICANT: Jackson, Paul J

APPLICANT: Lennert, Bruce E

TITLE OF INVENTION: Receptors

FILE REFERENCE: S-89,662

CURRENT APPLICATION NUMBER: US/09/273,839A

CURRENT FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 1.2

SOSTWARE: PatentIn Ver. 2.0
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                                     EKVIGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTS
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     EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTS
                                                                                               RTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD
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                                                                                                                                                                                                                                                                                                                                  421 APIALNAQDDFSSTPITMN------
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US-09-273-839A-8
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US-09-273-839A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSETRIISKNISISRIHISEVHONAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
20.7%; Score 781; DB 3; Length 881;
Best Local Similarity 30.4%; Pred. No. 1.4e-46;
Matches 245; Conservative 134; Mismatches 298; Indels 130;
                 CITY.

STATE: FL
COUNTRY: US

ZIP: 32606-6669

COMPUTER READBALE FORM:

MEDIUM TYPE: FLORDY disk
COMPUTER: IEM PC compatible
OPERATURE: IEM PC compatible
OPERATURING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
ATTORNEY/ADENT INFORMATION:
APPLICATION NUMBER: 39.355
REGISTRATION NUMBER: 39.355
REGISTRATION NUMBER: 39.355
REGISTRATION NUMBER: 39.355
REGISTRATION NUMBER: 35.375-8100
TELEPHONE: 352-375-8100
TELEPHONE: 352-375-8100
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TELEPHONE: BERNOCK/PORCET UND SACONT TELEPHONE: STANDAL SACONT SACONT TELEPHONE: STANDAL SACONT SACONT TELEPHONE: STANDAL SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACONT SACON
: 2421 N.W. 41st Street, Suite A-1 Gainesville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG 626
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              655 VINDRYDMINI--SSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSE 712
                                                                                                                                     SD--TKFNIDSKTFKELKLFKIDSQNQPQQDGDELRNPEFNKKESQBFLAKPSKINLFT 212
                                                                                                                                                                                                                                                                                                                                                    DSETRIISKATSISRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 VAQE--WGISIGNISQFNIASAGYLNANVRYNNVGIGAIYDVKPIISFVL-NNDIIAII 420
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                                                                                                                                                                                                   SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                                                                            213 OKMKKEIDED----TÖTDGDSIPDLWEENGYTI----ONRIAVKWDDSL-ASKGYTKFVSN 264
                                                                                                                                                                                                                                                                                                                PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 ----NSVESHSSTNWSYT-----NTE-----GASVEAGIGPKGISFGVSVNYQHSET 363
  456 YGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE
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APPLICANT: Downer, David
APPLICANT: Dullum, Charles Joseph
APPLICANT: Mulm, Charles Joseph
APPLICANT: Stamp, Lisa
APPLICANT: Finstad-Lee, Stacey
APPLICANT: Finstad-Lee, Stacey
APPLICANT: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 144
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----LUTINID----KDIRKITSGYIVEIEDTE-----
                                                                                           RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKQKSS
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Schnepf, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeits, James
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APPLICANT: Feitele
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US-09-073-898-32
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US-09-107-106-8
; Sequence 8, Application US/09307106
; Patent No. 663030
; Patent No. 663030
; APPLICANT: Feitelson, Jerald S. APPLICANT: Schnepf, H. Ernest APPLICANT: Schnepf, H. Ernest APPLICANT: Schnepf, H. Ernest Schneiber, David APPLICANT: Schnepf, Brian A. APPLICANT: Schnepf, Brian A. APPLICANT: Schneiber, David APPLICANT: Muller-Cohn, Judy APPLICANT: Muller-Cohn, Judy APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Stamp, Lisa APPLICANT: Sequences Which Encode These Toxins NUMBER OF SEQUENCES: 54
CORRESPONDENCES: 54
CORRESPONDENCES: 54
CORPUTER: FL
COUNTRY: US
STREET: 2421 N.W. 41st Street, Suite A-1
STATE: FL
COUNTRY: US
COMPUTER: PLOPPY disk
COMPUTER: IBM PC Compatible
CORPUTER: IBM PC Compatible
CORPUTER: IBM PC-DOS/WS-DOS
SOUTHARE: BACHTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/307,106
FILING DARE:
CLASSIFFATATION
FILING DARE: 713 NGDT-STNGIK---KILIFSKKGYEIG 735 764 IKQIYSRYGİKLEDGİLİDKKGĞIHYĞ 790 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/073,898
FILING DATE: US-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANGETS, ASY
REGISTRATION NUMBER: 39,355 456 481 516 g g d ò Db $\overset{>}{\circ}$ ò ò à

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536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKENOLSQILAPNNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTQNT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 TTKPDMTLKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537 KT-PSLTLKDALKLSYPDEIKEIEGLLYYKNKPIYESSUMTYLDENTAKEVTKQLNDTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---NATNIYTVLDKIKLNAKANILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             596 KFKDVSHLYDV----KLTPKANVTIK-LSILYDN---AESNDNSIGKWTNTNIVSGGNNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSETRIISKNISISRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS
                                                                                                                                                                                                                                                                                                                                                                                                       SRKKRSTSAGPTVPDRDNDGI PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS
                                                                                                                                                                                                                                                                                                                                                                                                                        213 QKMKREIDED---TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN
                                                                                                                                                                                                                                               4 QENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                Query Match

20.7%; Score 781; DB 4; Length 881;
Best Local Similarity 30.4%; Pred. No. 1.4e-46;
Matches 245; Conservative 134; Mismatches 298; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                     122 RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPFLKQKSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      713 NGDT-STNGIK---KILIFSKKGYBIG 735
REFERENCE/DOCKET NUMBER: MA-708C2
TELECOMMUNICATION INFORMATION:
TELEPAN: 352-375-8100
TELEPAN: 352-375-800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERICTICS:
LENGTH: 881 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: PSI77C8a
                                                                                                                                                                 ;
US-09-307-106-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283
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321 ----NSVESHSSTNWSYT-----NTE------GASVEAGIGPKGISFGVSVNYQHSET 363
                                                                                                                                                                                                                                                                                                                                                340 LAGERTWAETMG----LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATIK 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 655 VINDRYDMLNI--SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSE 712
                                                                                                                                        213 ÇKWKREIDED---TÜTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN 264
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95 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                           223 PEKWSTASDPYSDFEKVTGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                      283 DSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
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Morrill, George
Morrill, George
INVENTION: No. 6656908el Pesticidal Toxins and Nucleotide
Sequences Which Encode These Toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
20.7%; Score 781; DB 4; Length 881;
Best Local Similarity 30.4%; Pred. No. 1.4e-46;
Matches 245; Conservative 134; Mismatches 298; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                 Sequences miles

NUMBER OF SEQUENCES: 144

CORRESPONDENCES: 144

CORRESPONDENCES: 144

CITY: Gainesville
CITY: Gainesville
CITY: Gainesville
STATE: FL

COUNTRY: US

COMPUTER: FL

COMPUTER: FLOPPY disk

COMPUTER: TEMP CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTEN PC-DOS/MS-DOS
SOFTWARE: TEMP CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTENCE OF MAY-2001
CURRENT APPLICATION NUMBER: US/09/850,351A
FILING DATE: 07-May-2001
CLASSIFICATION NUMBER: US 09/073,898
FILING DATE: 06-MAY-1998
APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1997
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: SANGETS JS-372-5800
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
    764 IKQIYSRYGIKLEDGILIDKKGGIHYG 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INDIVIDUAL ISOLATE: PS177C8
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-850-351A-32
                                                                                                                                                  APPLICANT: Feitelson, Jerald S.
Schnepf, H. Ernest
Narva, Kenneth E.
Stockhoff, Brian A.
Schmeits, James
Loewer, David
Dullum, Charles Joseph
                                                         RESULT 13
US-09-850-351A-32
Sequence 32, Application US/09850351A
Setent No. 6656908
GENERAL INFORMATION:
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RESULT 14

US-08-471-033-5

Sequence 5, Application US/08471033

Sequence 5, Application US/08471033

Sequence 5, Application US/08471033

Sequence 5, Application US/08471033

Septimal INFORMATION:

APPLICANT: Warren, Gregory W
APPLICANT: Millins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Nye, Gordon J
APPLICANT: Notional B
APPLICANT: Dock, Nicholas B
APPLICANT: Beruch, Juan J
APPLICANT: Beruch, Juan J
APPLICANT: Beruch, Juan J
APPLICANT: Beruch, Juan J
APPLICANT: Carr. Stian

STREET: 7 Skyline Drive
CITY: Hawthorne

STREET: 7 Skyline Drive
CITY: Hawthorne
STREET: NY
COUNTRY: USA
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SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ 121

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34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGNIATYNFENGRVRVDIGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
20.6%; Score 779; DB 1; Length 884;
Best Local Similarity 30.3%; Pred. No. 1.9e-46;
Matches 247; Conservative 129; Mismatches 293; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 QENRILINESESSSQGLILGYYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                               FILIND DATE:

CLASSIFICATION: 530

RIOR APPLICATION: 530

RIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594

FILING DATE: 09-SEP-1994

FILING DATE: 09-SEP-1994

FILING DATE: 23-MAR-1994

FILING DATE: 23-MAR-1994

RIOR APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: CGC 1695/CIP3/DIV7 - SQLv3

TELECHMONICATION INFORMATION:

TELEPHONE: 919-541-8689

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

TEMMOTH: RAR ANTHON STICS:
ZIP: 10532
MEDIUM TYPE: FLORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OS/471,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 884 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-471-033-5
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S)	OY SIG LINE DISTORAGE OF CO.		3
ជ	Db 540 KT-PSLTLKDALKLSYPDEI	- PSLTLKDALKLSYPDEIKEIEGLLYKRNKPIYESSVMTYLDENTAKEVTKOLNDTTG	598
ő	Cy 570NATNIYTVLDKIKLNAK	-NATNIYTVLDKIKLNAKMYILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG	626
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ő	Qy 627LLLNID	KDIRKILSGYIVEIEDTEGLKE	654
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ជ	Db 761.NLTDSBIKQIYSRYGIKLEDGILIDKKGGIHYG	BDGILIDKKGGIHYG 793	
R	RESULT 15		
5	Sequent Patent	1044	
- ^-	INFORMATION:		
	Koziel, N	z (II)	
٠. ٠	Mullins, Martha		
	; APPLICANT: Carr, Brian		
٠. ٠	, APPLICANT: Desai, Nalini M appl. roant) 1	
•••	Duck, Nichola	n	
•- •	Estruch,	1868el Pesticidal Proteins and Strains	
	SEQUENCES: 50		
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	a: CibA-Gaigi 7 Skyline Driv	corporation e	
~	awt		
	STATE: NY CONNERS . 1158		
	; ZIP: 10532		
• • •	EADABLE FORM:		
•- •	E: Flor IBM PC	w	
	SYSTEM: P	-DOS	
•• ••	- 2	8 #1.0, Version #1.308	
	APPLICATION NUMBER: US/08/	/471,044	
	; FILING DATE: 06-JUN-1995 ; CLASSIFICATION: 800		
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	; APPLICATION NUMBER: US 08, ; FILING DATE: 05-JUN-1995	/463,483	
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•- •	; APPLICATION NUMBER: US 08,	/314,594	
	; PRIOR APPLICATION DATA:		
•• ••	JS 08	/218,018	
	}		
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	, ATTORNEY/AGENT INFORMATION:		
	ум. ВЕR: 40,4		
	KET NUMBER:	CGC 1695/CIP3/DIV6 - SQLv3	
٠	919-		
•	919-541-868		

9

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20.6%; Score 779; DB 2; Length 884;
Best Local Similarity 30.3%; Pred. No. 1.9e-46;
Matches 247; Conservative 129; Mismatches 293; Indels 146; Gaps information for SEQ ID NO: 5:
 SEQUENCE CHARCTERISTICS:
 IENGTH: 884 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECTLE TYPE: protein
US-08-471-044-5 223 셤 ઠે dd ò 엄 à ò g à 유 ò 셤 $\stackrel{>}{\circ}$ 원 ò 쉱 δ g ò à

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S99 KFKDVSHLYDV----KLTPKANVTIK-LSILYDN----AESNDNSIGKWTNTNIVSGGNNG 650 570 ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG ------LLLNID-----KDIRKILSGYIVEIEDTE------GLKE

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us-09-848-909a-8.rapb

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May 3, 2004, 19:40:13 ; Search time 36.6393 Seconds (without alignments) 5560.545 Million cell updates/sec
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3773
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3: /cgn2_6/prodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/prodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/prodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/prodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/prodata/2/pubpaa/USO8_NEW_PUB.pep:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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RESULT 1 US-10-410-647-30 Sequence 30, Application US/10410647 Publication No. US20030235816A1 GENERAL INFORMATION: APPLICANT: PLEXUS VACCINE, INC. APPLICANT: PACTICE, V8evolod APPLICANT: Bordner, Andrew APPLICANT: Bordner, Andrew APPLICANT: Deans, Robert APPLICANT: Bordner, Mary TITLE OF INVENTION: IMMUNOGENIC PEPTIDES, FILE REFERENCE: PLEXILIO. TUTLE OF INVENTION: IMMUNOENIC PEPTIDES, FILE REFERENCE: PLEXILIO. CURRENT APPLICATION NUMBER: US 60/373,668 PRIOR FILING DATE: 2002-04-08 PRIOR FILING DATE: 2002-04-08 PRIOR PLING DATE: 2002-04-08 NUMBER OF SEQ ID NOS: 46 SOFTWARE: PACE OF SEQ ID NOS: 46 SOFTWARE: PACE OF SEQ ID NOS: 46 SOFTWARE: PACE OF SEQ ID NOS: 46 SOFTWARE: PACE OF SEQ ID NOS: 46 SOFTWARE: PACE OF SEQ ID NOS: 46 SOFTWARE: PRICE OF SEQ ID NOS: 4	Query Match Best Local Similarity	Matches			
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                                                                 OSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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US-99-848-909-2
Sequence 2, Application US/09848909
Sequence 2, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: COllier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT FILING DATE: 2001-05-04
PRICR TRILING DATE: 2001-05-04
PRICR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
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Pred. No. 4.5e-274;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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TYPE: PRT
ORGANISM: Bacillus anthracis
US-09-848-909-1
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Pred. No. 4.5e-274;
0; Mismatches 1;
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                 4.0
) NUMBER OF SEQ ID NOS: 35
) SOFTWARE: FaetSEQ for Windows Version
) SEQ ID NO 3
| LENGTH: 736
| TYPE: PRT
| TYPE: PRT
| GGANISM: Bacillus anthracis
US-09-848-909-3
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US-09-848-909-4
US-09-848-909-4
Sequence 4, Application US/09848909
; Publication No. US20020039588A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Sellman, Brett R.
; TITLE OF INVENTION: Compounds and Met
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US-09-846-909-3

Sequence 3, Application US/09848909;
Publication No. US20020039588A1

GENERAL INFORMATION:
APPLICANT: Collier, R. John

TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REFERRNCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800
                                                         Indels
                            Score 3767; DB 12;
Pred. No. 4.5e-274;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 734; Conservative
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                                                                                                                                                                                           Length 736;
TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: 02/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR PPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                          Ouery Match
99.8%; Score 3767; DB 12;
Best Local Similarity 99.9%; Pred. No. 4.5e-274;
Matches 734; Conservative 0; Mismatches 1;
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                                                                                                                                       ; TYPE: PRT; ORGANISM: Bacillus anthracis
US-09-848-909-4
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Sequence 5, Application US/09848909
; Publication Wo. US20020039588A1
; GARERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Callier, R. John
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: UNMERS: US/09/0848,909
; CURRENT FILING DATE: 2001-05-04
; RELOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 736
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ORGANISM: Bacillus anthracis
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                                                                     Fublication No. US2020039588A1

Publication No. US2020039588A1

GENERAL INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Collier, R. John

ITILE OF INVENTION: Compounds and Methods for the Treatment

ITILE OF INVENTION: and Prevention of Bacterial Infection

ITILE OF INVENTION: and Prevention of Bacterial Infection

CURRENT APPLICATION NUMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 736
                                                                                                                                                                                                                                                                                                                                    Length 736;
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Pred. No. 4.5e-274;
0; Mismatches 1;
721 IKKILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.9%;
Matches 734; Conservative
                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-09-848-909-6
                                                 RESULT 7
US-09-848-909-6
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; Publication No US200200395881
; GENERAL INFORMATION:
; APPLICANT: COLlier. R. John
; APPLICANT: COLlier. R. John
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR APPLICATION NUMBER: US 60/201,800
; NUMBER OF SEQ ID NOS: 35
; SOG ID NOS: 35
; SEQ ID NOS: 35 Length 736; Indels Query Match
99.8%; Score 3767; DB 12;
Best Local Similarity 99.9%; Pred. No. 4.5e-274;
Matches 734; Conservative 0; Mismatches 1; IKKILIFSKKGYEIG 735 IKKILIFSKKGYEIG 735 ; TYPE: PRT; ORGANISM: Bacillus anthracis US-09-848-909-7 RESULT 8 US-09-848-909-7 LENGTH: 736 361 561 199 721 721 61 121 181 421 421 481 541

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Tue May

Qy 481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540 481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540 Qy 541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 600 Qy 601 NNIAVGADESVVKEAHREVINSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 Qy 601 NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 Qy 661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNYYAVTKENTIINPSENGDTSTNG 720 Qy 661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNYYAVTKENTIINPSENGDTSTNG 720 Qy 721 IKKILIFSKKGYEIG 735 Db 721 IKKILIFSKKGYEIG 735 y 8equence 9, Application US/09848909 ; Sequence 9, Application US/09848909 ; Changal 100 Changal 100	APPLICANT: Collier, R. John APPLICANT: Collier, R. John APPLICANT: Collier, Brett R. TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection FILE REPREMEER: 00742/060002 CURRENT APPLICATION NUMBER: US/09/848,909 CURRENT FILING DATE: 2001-05-04 NUMBER OF SEQ ID NOS: 35 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 736 TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT TYPE: PAT	imilarity Conser EVKQENKLL EVKQENKLL EVKQENKLL	Db 61 QSAIWSGFIKUKKSDEYTFATSADNHVIMWVDDGEVINKASNSNKIRLEKGRIYQIKKLOY 120 QY 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKGRSTSAGFTVPDRDN 180 121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKGRSTSAGFTVPDRDN 180 QY 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKYT 240 Db 191 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKYT 240 QY 241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 300 241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 300 QY 241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 300 QY 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 360 QY 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 360 QY 361 NANIRYVNTGTAPIYNVLFTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 220
Db 541 QYQGXDITEFDFWFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKANILLIRDKRFHYDR 600 Qy 601 NNIAVGADESVVKEAHREVINSSTEGLLANDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 Db 601 NNIAVGADESVVKEAHREVINSSTEGLLANDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 Qy 661 DALNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKNVYAVTKENTIINPSENGDTSTNG 720 Gy 661 DALNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKNVYAVTKENTIINPSENGDTSTNG 720 Qy 721 IKKILIFSKKGYEIG 735 Db 721 IKKILIFSKKGYEIG 735 RESULT 9 YS-09-848-90-8 S Squence 8, Application US/09848909 PUS-09-848-90-8 S Squence 8, Application US/09848909 PUS-101 IKKILIFSKKGYEIG 735 TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment FILE REPERRENCE: 0742/060012	CURRENT FILING DATE: 2011-05-04 PRIOR APPLICATION NUMBER: US 60/201,800 PRIOR FILING DATE: 2000-04-04 NUMBER OF SEQ ID NOS: 35 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 8 LENGTH: 736 CORGANISM: Bacillus anthracis US-09-848-999-8 Query Match Best Local Similarity 99.8%; Fred. No. 4.5e-274; Matches 734; Conservative 0; Mismatches 1; Indels 0, Gaps 0;	OY 1 EVKQENELLARSESSQQLLGYYFSDLARQAPMVTSSTTGDLSIPSSELENIPSENQYF 60 1 EVKQENELLARSESSSQQLLGYYFSDLARQAPMVTSSTTGDLSIPSSELENIPSENQYF 60 QY 61 QSAIWSGPIKVKKSDEYTFATSADNHYTMWVDDQEVINKASNSKIRLEKGRLYQIKIQY 120 Db 61 QSAIWSGPIKVKKSDEYTFATSADNHYTMWVDDQEVINKASNSKIRLEKGRLYQIKIQY 120 QY 121 QRENPTEKGLDFLYWTDSQUKKEVISSDNLQLPELKQXSNNSKIRLEKGRLYQIKIQY 120 QY 121 QRENPTEKGLDFLYWTDSQUKKEVISSDNLQLPELKQXSNNSKIRRSTSAGPTVPDRDN 180 DD 121 QRENPTEKGLDFKLYWTDSQUKKEVISSDNLQLPELKQXSSNSRKKRSTSAGPTVPDRDN 180	Oy 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKMSTASDPYSDFEKVT 240 181 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKMSTASDPYSDFEKVT 240 241 GRIDKNVSPEARHELVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 300 Qy 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360 Db 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 360 Qy 301 NANIRYVNTGTAPITYULPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 420 Qy 361 NANIRYVNTGTAPITYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 420 QV 421 LNAQKDFSSTPITWNYNOFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480 421 LNAQKDFSSTPITWNYNOFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480

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121. ÖRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180
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US-09-646-909-11
US-09-646-909-11
Sequence 11, Application US/09948909
Publication No. US202020039588A1
GENERAL INPORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: And Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
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SEQ ID NO : 35
TENDENCE: PRESERVE PRESERVE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREESE FREES FREESE FREESE FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FREES FR
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Pred. No. 4.5e-274;
0; Mismatches 1;
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CRGANISM: Bacillus anthracis
US-09-848-909-11
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Matches 734; Conservative
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Sequence 10, Application US/09848909
Sequence 10, Application US/09848909
Publication Wo. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEC ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 736
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Pred. No. 4.5e-274;
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DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKOVSPEARHPLVARYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT	301 SEVAGNAEVHASFEDIGGSVSAGFSNSNSTVAIDHSLSLAGEETWAETWOLNTADTARL 360 301 SEVAGNAEVHASFEDIGGSVSAGFSNSNSSTVAIDHSLSLAGEETWAETWOLNTADTARL 360 301 SEVAGNAEVHASFEDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWOLNTADTARL 360 361 NANIRYVNTGTAPTYNVLPTTSLVLGKNOTLATIKAKENOLSQILAPNNYYPSKNLAPIA 420 361 NANIRYVNTGTAPTYNVLPTTSLVLGKNOTLATIKAKENOLSQILAPNNYYPSKNLAPIA 420	LINAQKDESSTPITMNYNQELELEKTKOLRLDTQVYGNIATYNFENGRYRVDTGSNWSEV		601 NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660	661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNYYAVTKENTIINPSENGDTSTNG 720 721 IKKILIFSKKGYEIG 735 721 IKKILIFSKKGYEIG 735	13 18-909-12 nce 12, Application US/09848909 nation No. US20020039S88Al	APPLICANT: Collier, R. John APPLICANT: Collier, R. John APPLICANT: Sellman, Bett R. AITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection OTAL OF INVENTION: and Prevention of Bacterial Infection TITLE OF INVENTION: 00742/060002 CURRENT APPLICATION NUMBER: US/09/848,909 CURRENT APPLICATION NUMBER: US 60/201,800 PRIOR PILING DATE: 2000-04-04 PRIOR PILING DATE: 2000-04-04 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 12 LENGTH: 736 TYPE: PRT ORGANISM: Bacillus anthracis US-09-848-909-12 Query Match Back Local Similarity 99.9%; Pred. NO. 4.5e-274; Masches 734: Concertative 1.	ESSSQGLLGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENGYF 60 ESSSQGLLGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENGYF 60 ESSSQGLLGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENGYF 60 KSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 12 KSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 12

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601 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
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RESULT 15
US-09-848-909-14
Sequence 14, Application US/09848909
Sequence 10. Application US/09848909
Publication No. US20202039588A1
GENERAL INFORMATION:
APPLICANT: COllier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
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TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: 2014/060002
CURRENT APPLICATION NUMBER: US/09/846,909
PRIOR APPLICATION NUMBER: US/09/846,909
PRIOR APPLICATION NUMBER: US/09/846,909
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Search completed: May 3, 2004, 20:02:04 Job time : 53.6393 secs

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99.8%; Score 3767; DB 12; Length 736; arity 99.9%; Pred. No. 4.5e-274; onservative 0; Mismatches 1; Indels 0; Gaps	SESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 6	NELLNESESSSGGLLGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENQYF 6	SGFIKVKKSDEYTFATSADNHVTWAVDDQEVINKASNSNKIRLEKGRLYQIKIQY 12	SGFIKVKKSDEYTFATSADNHVTMMVDDQEVINKASNSNKIRLEKGRLYQIKIQY 12	FKLYWIDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 18	SQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 18	KKGLTKYKSSPEKWSTASDPYSDFEKVT 24	SYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT 24	SPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHT 30	SPBARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 30		SNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARL 36	42	PNNYYPSKNLAPIA 42	SSTPITMNYNOFLELEKTKOLKLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 48	SSTPITMNYNÖFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 48	DETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEBNGNL 54	SETTARIIENGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 54	YTVLDKIKLNAKMNILIRDKRFHYDR 60	TEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 60	KILSGYIVEIEDTEGLKEVINDRY 66	regikevindry 66	SSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 72	SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 72	IFSKKGYEI	LIPSKKGYEIG 735
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Sequence 8, Application PC/TUS0335733

Sequence 8, Application PC/TUS0335733

GENERAL INFORMATION:

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE REPRESENCE: 0742/072003

CURRENT FILING DATE: 2003-10-10

PRIOR PILING DATE: 2003-10-10

PRIOR FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 735
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US-09-848-909A-8

PCT-US03-35733-6

US-09-848-909A-7

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PCT-US03-35733-10

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PCT-US03-35733-21

US-09-848-909A-10

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Best Local Similarity 100.0%; Pred. No. 5e-299;
Matches 735; Conservative 0; Mismatches 0;
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   3, 2004, 19:36:13 ; Search time 175.546 Seconds (without alignments) 4086.665 Million cell updates/sec
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US-09-848-909A-8
| SQUENCE 8, Application US/09848909A
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| SARINGANATION:
| APPLICANT: Collier, R. John
| APPLICANT: Collier, R. John
| TITLE 0F INVENTION: and Prevention of Bacterial Infection FILE REPERENCE: 00742/060002
| CURRENT APPLICATION: NUMBER: US/09/848,909A
| CURRENT PILING DATE: 2001-05-04
| NUMBER OF STO ID NOS: 35
| SOFTWARE: FRACESQ for Windows Version 4.0
| SEQ ID NO 8
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment:
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/07203

CURRENT APPLICATION NUMBER: PCT/US03/35733

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: US 60/424,987

PRIOR FILING DATE: 2002-11-08

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FASTERO for Windows Version 4.0
    Length
Query Match
100.0%; Score 3773; DB 23; Length
Best Local Similarity 100.0%; Pred. No. 5e-299;
Matches 735; Conservative 0; Mismatches 0; Indels
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                                                                      Length 735
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                                                                      Score 3769; DB 1;
Pred. No. 1.1e-298;
1; Mismatches 0;
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Best Local Similarity 99.9%;
Matches 734; Conservative
                      TYPE: PRT CRGANISM: Bacillus anthracis PCT-US03-35733-7
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Sequence 7, Application US/09848909A
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Seliman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REPERRING: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
RESULT 4
US-09-848-909A-7
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Sequence 6, Application PC/TUS0335733 GENERAL INFORMATION: APPLICANT: President and Pellows of Harvard

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                                                                                                                                                Indels
                                                                                                                       Score 3769; DB 23;
Pred. No. 1.1e-298;
1; Mismatches 0;
CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: US 60/201,800

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SEQ ID NO 7

LENGTHARE: PattSEQ for Windows Version 4.0

LENGTH: 735

TYPE: PRT

ORGANISM: Bacillus anthracis
US-09-848-909A-7
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Best Local Similarity 99.9%;
Matches 734; Conservative
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PCT-US03-35733-6
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Sequence 6, Application US/09848909A; Sequence 6, Application US/09848909A; General Information: John Applican: Collier, R. John Applican: Collier, R. John TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection TITLE OF INVENTION: UNMER: US/09/848,909A; CURRENT APPLICATION NUMBER: US/09/848,909A; PRIOR FILING DATE: 2000-05-04; NUMBER OF SEQ ID NOS: 35 SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ ID NO 6; SEQ 
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Pred. No. 1.3e-298;
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Best Local Similarity 99.9%;
Matches 734; Conservative
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
APPLICANT: President and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00/42/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT PILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
ENGTH: 735
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Pred. No. 1.6e-298;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 734; Conservative
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PCT-US03-35733-10
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Sequence 5 Application PC/TUS0335733

GENERAL INPORMATION:

TILE OF INVENTION: Compounds and Methods for the Treatment

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TILE OF INVENTION: Compounds and Methods for the Treatment

TILE OF INVENTION: Compounds and Methods for the Treatment

TILE OF INVENTION: Compounds and Methods for the Treatment

FILE REFERENCE: 0742/072003

CURRENT APPLICATION NUMBER: PCT/US03/35733

CURRENT FILING DATE: 2003-11-08

NUMBER: OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 735
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Pred. No. 1.6e-298;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 734; Conservative
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; TYPE: PRT
; ORGANISM: Bacillus anthracis
PCT-US03-3573-5
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(GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
APPLICANT: President and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFRENCE: 00742/03203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 735
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Pred. No. 1.6e-298;
0; Mismatches 1;
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Conservative
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ORGANISM: Bacillus anthracis
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TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REPERBYCE: 00742/072003;
CURRENT FILING DATE: 2003-10-10
FRIOR APPLICATION NUMBER: DCT/US03/35733
CURRENT FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 735
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Pred. No. 1.6e-298;
0; Mismatches 1;
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PCT-USO3-35733-20
Sequence 20, Application PC/TUS0335733
GENERAL INFORMATION:
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Best Local Similarity 99.9%;
Matches 734; Conservative
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Db 481 LPQ1QETTARIIFNGXDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNBPNGNL 540 OY 541 QYQGXDITEPDFNFDQQTGQNIXNQLAELNATNIYTVLBXIKLNAKMNLIRDKRFHYDR 600	Db 541 QYQGXDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDXIKLNAKMNILIRDKRFHYDR 600	CY 601 NNIAVGADESVVKEAHREVINSSTEGLLANDKDIRKILSGYIVEIEDTEGLKEVINDRY 660	CY 661 DMINISSLRODGKTFIDFKKKNDKLPLYISNPNYKNNVYAVTKENTIINPSENGDTSTNG 720	Qy 721 IKKTLIFSKKGYEIG 735 Db 721 IKKILIFSKKGYEIG 735	RESULT 11 US-09-791-537-43735 ; Sequence 43735, Application US/09791537		; LENGTH: 735 ; TYPE: PRT ; ORGANISM: pdb 1ACC US-09-791-537-43735	Query Match Best Local Similarity 99.8%; Score 3767; DB 22; Length 735; Best Local Similarity 99.9%; Pred. No. 1.6e-298; Matches 734; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 1 BUKQENRILNESESSQGLLGYYFSDLMFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60	Oy 61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNKIRLEKGRLYQIKIQY 120 	OY 121 ORENPTEKGLDFKLYWTDSONKKEVISSDNLOLPELKOKSSNSRKKRSTSAGPTVDDRDN 180	OY 181 DGIPDSLEVECYTVDVKNKRTFLSPWISNIHEKKGLIKYKSSPEKWSTASDPYSDFEKVT 240	Qy 241 GRIDKNVSPBARHPLVAAYPIVHVDWENIILSKNEDQSTQNTDSETRTISKNTFT 300	QY 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERFWAETMGLNTADTARL 360	Qy 361 NANIRYUNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 420	OY 421 LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480

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US-09-848-909A-21
S-09-848-909A-21
S-GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REPRENCE: 00742/06002
CURRENT FILING DATE: 2001-05-04
FRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
IBNGH: 735
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US-09-848-909A-21
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            g
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Search completed: May 3, 2004, 19:57:37 Job time : 190.546 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 3, 2004, 19:30:47; Search time 13.0855 Seconds (without alignments) 5403.004 Million cell updates/sec Run on:

US-09-848-909A-8 3773 1 EVKQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 735 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

283366 Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protective antigen	in	cryptic protein -	ical			Ē	y pro	ij		Sno	O		ized p	prot	cat	hypothetical prote	a]	al	<u> </u>	cal p	tein - My	cal p	like out	organel:	alpha-toxin - Clos	201	Je	ü
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ALIGNMENTS

RESULT 1

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	tive antigen r
	2001-111-01 205
	C.Date: 19-011-1990 Hedguence Fevision 19-011-1990 #reac_change vi-bec-2000 C.accosion 139934: 869160: P59104
	R; Welkos, S.L.; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J.
	A_Title: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthr a nosetance number, 130033. MITD.80170073. PMID.3148491
	A; Accession: 139934
	A;Status: preliminary; translated from GB/EMBL/DDBJ
	A;Cross-references; GB:M22589; ND105143280; PIDN.AAA2287.1; PID19143202 A;Cross-references; GB:M22589; ND105143280; PIDN.AAA2287.1; PID19143202
	A, Title: In vitro processing of anthrax toxin procective antigen by recombinant PC1 (SF
	A;Kelgefance indimber: Sosiov; MulD:951*20/v; FMLD:/04/05/ A:Apropasion: 869160
	A; Molecule type: protein
,	R.Okinaka, R.T.; Cloud, K.; Hampton, O.; Holimaster, A.K.; Hill, K.K.; Kelm, F.; Kohile
	O. Sacterior: 191, 9379-9315, 1399 A:Tile: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbor
	A59091; MUID: 99445483; PMID: 10515943
	A.Accession: F59104
_	A;Status: preliminary
	A; Molecule type: DA, A15_764 CAXTS
	A: Cross.references: (B: AF065404; NID: 04894216; PIDN: AAD32414.1; PID: 94894326
	A, Note: similar to anthrax toxin moiety, protective antigen, pagA formerly pag, plasmid
	C;Genetics:
	A Jene: DA1-110
	Ajdentille: plasmid
	to receptors on
	y active components edema factor or lethal factor; the complex is internalized by recep
	C; Keywords: exotoxin
	Fil-29/Domain: signal sequence #status predicted <sig></sig>
	F.30-196/Domain: propedition Hatatus predicted a Arko.
-	1
	Query Match 99.8%; Score 3767; DB 2; Length 764;
	0
	Qy 1 BVKQENRLIANESESSQGLLGYYFSDLARQAPMVVTSSTTGDLSIPSSELENIPSENQYF 60
_	DD 3.0 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVISSITGDLSIFSSELENIFSERUXFF 0.9

	QSAIWSGFIKVKKKUDEYIFAISANNHVIWWVDDEFYINAASNNNKIKHEKKKRIGIALUI 149 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQIPELKQKSSNSRKKKSTSAGFTVDRDN 180 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQIPELKQKSSNSRKKSSTSAGFTVDRDN 209		. Ag	95 IKŚIRWIĠRIIPSEDGĖYILSTDR-NDVLMQINAKGDIAKTLKVNMKKGQAYNIRIE 150 120 YQRENPTEKGLDFKLYWIDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTS 170 121 IQDKNLGSIDNLSVPKLYW-ELNGNKTVIPEENLFPRDYSKIDEND 195
181 DGIPDSLEVEGYTVDVKNKR 			୍ଦ ଶ	171 AGPTVP
241 GRIDKOVSPEARHPLVAAYP 	GRIDKAVVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300 		oy Oy	212 EKKGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIIL 271 : : : : :
301 SEVHGNAEVHASFFDIGGSV 	SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 360 	-	& a	272 SKNEDQSTQNTDSETRTISKNISTSRTHISBYHGNAEVHASFFDIGGSVSACFSNSNSST 331 : : : : : : : : :
361 NANIRYVNTGTAPIYNVLPI 	NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 420 	-	o S	332 VAIDHSLSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSL 383 : :
Qy 421 LNAQKDPSSTPITMAYNQFI	INAQKDFSSTPITMAYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480		ý q	384 VLCKNOTLATIKAKENOLSQILAPNNYYPSKNIAPIALNAQKDFSSTPITMNYNQFLELE 443
Qy 481 LPQIQETTARIIFNGKDLNI 	LPQIQETTARIIFNGKOLNLVERRIAAVNPSOPLETTKPDMTLKEALKIAFGFNEPNGNL 540 		\$ 8	444 KTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVER 503
Oy 541 QYQKDITEFDFNFDQQTS(qyqgkditefdfnfdqqtsqnikaqlaelnatniytvldkiflnakmnilirdkrfhydr 600 		& 8	504 RIAAVNPSDPLETTKPDWILKEALKIAFGFNEPNGNLQY-QGKDITEFDFNFDQQTSQ 560
Qy 601 NNIAVGADESVVKEAHREVT 	NNIAVGADESVVKEAHREVINSSTEGLLLANIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 		co Op	561 NIKNGLAELNATNIYTYLDKIKLNAKONILIRDKRFHYDR-NNIAVGADESVVKBAHR 617
Qy 661 DMLNISSLRQDGKTFIDFKI 	DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720 		ò 8	618 EVINSSTECLLLNIDKDIRKILSGYIVELEDTEGLKEVIND 658 :
Oy 721 IKKILIFSKKGYEIG 735 	-	-	Qy Dp	659 RYDMINIS SLRQDGKTFIDFKKYNDKLPLYISNPNYKV 696
RESULT 2 140862 140862 1540862 155pecies: Clostridium perfringens C;Species: Clostridium perfringens C;Species: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text C;Accession: 140862; 842774 R;Perelle, S: Gibert, M: Boquet, P: Popoff, M.R. Infect. Immun. 61, 5147-5156, 1993 A;Title: Characterization of Clostridium perfringens iot A;Reference number: 140861; MUID:94041637; PMID:8225592 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: 140862 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-975 <res> A;Cross-references: BMBL:X73562; NID:g929031; PIDN:CAA5: A;Cross-references: BMBL:X73562; NID:g929031; PIDN:CAA5: Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les Best Local Similarity 31.2%; Score 877; DB 2; Les</res>	omponent Ib - Clostridium perfringens lostridium perfringens ug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999 ug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999 ug-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999 .; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Boquet, P.; Popoff, M.R; Gibert, M.; Popoff, M.R; Gibert, M.; Popoff, M.R; Gibert, M.; Gibert, M.; DBD, M.;	ion in	Qy Db RESULT 3 139933 139933 139933 Cryptic C, Date: C, Date: C, Access R, Welkos R, Welkos A, Access A, Access A, Access A, Access A, Access A, Access A, Access A, Cross- Ouery Best I	Oy 697NVYAVTKENTIINPSENGDFSTNGI 721 Db 760 ILDAHNKYADIKLDTNTGNTYIDGI 785 RESULT 3 Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic protein - Bacillus anthracis Cryptic Bacillus anthracis Cryptic Bacillus anthracis Cryptic Bacillus anthracis Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis articles: 1-192 ergs> Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis articles: 1-192 ergs> Article: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis articles: 1-192 ergs> Article: Sequence and Bacillus anthracis a

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rhoptry protein - Plasmodium yoelii (fragment)
C;Species: Plasmodium yoelii
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
C;Accession: T28676; A4551.
A;Sinha, K.A.; Keen, J.K.; Ogun, S.A.; Holder, A.A.
Mol. Blochem. Parasitol. 76, 329-332, 1996
A;Title: Comparison of two members of a multigene family coding for high-molecular of A;Reference number: Z20507; MUID:97077455; PMID:8920022
                                                                                                   3908 YQLLLSNLNSN------REYRFEKIBINHISNTNNFEDLEKLMGVSNTFITQTKNT 3957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4018 DVTSDFKEGTWAHDLSNSVNFKEETTYKLVKIQFVNKPTKAKNNINNSENNVLLDNINSI 4077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4078 NSNYEFTTKVGDHKLINİTSSNAVATNSQTINFTLSGVKKSAVGKKİKLSYKSADTSESI 4137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4258 YLTATIVDLNFN-DKVNIVNISFNNKPSIAAEN-----IGIDKSNNII-----YNNDS 4304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NDIIETNVINGSSLVNNDGKTSIRFTLNNLKANKLYSLVDVYYLVNNNSNTIVE 4415
                                                                                                                                                                                                                                                                                                                                                              3796 WLIKGQI----DNLN-PETKYKLENIELSKPLKTHTNLSVSINDKENISLITETGNPVLKV 3851
40;
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                                                                                                                                                                                                                                                                                                                                                                                                                           ----NDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEKVIGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKN-EDOSTONTDSET-RIISKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3958 TVQWNDSSATIVGTRGVNFNFKIKSEDKILENNQOVVAMFAPKETIRDTNTWLQYTRPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSLSLAGERTWAETWGLNT---ADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TIKAKENQLSQILAPNNYYPSKNLAPIALN-AQKDFSSTPITMNY--NQFLELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4138 HTNEVLIESNKTOYNILLNNLKRNRTYTLIDVKLIDNNNVSDFPKEGNLTNSFITTRTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INLVERRIAAVNPSDPLETT-----KPDMTLKEA------LKIAFGFNEPNGNLO
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                                                             19 LLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYT
                                                                                                                                                                                    PATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTD
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      324;
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A;Molecule type: DNA
A;Residues: 1-2401 <SIN>
      Mismatches
      Conservative 132;
      174;
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Cipace: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
Cipace: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
Cipacesion: G59104
Cipace: 12-Nov-1999 #sequence_revision of px01, Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehler
Cipacesion: G59104
A; Title: Sequence and organization of px01, http://dx.ic.io.com/anthracis/plasmid/harbori/A; Residues: Dreliminary
A; Accession: G59104
A; Residues: 1-204 < OKI>
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Cross-references: GB:AE002145; GB:AF222894; NID:g6899476; PIDN:AAF30894.1; GSPDB:GN001
Experimental source: serovar 3; biovar 1
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                                                                                                                                                                       60 KKPSNHLTNSPVTITLAGKDSGVGELYRVLS-----DGAGFLDFNKFDENWRSLV-DPG 112
            MNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI 646
                                                                                                                                647 EDTE------GLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPN 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein pXO1-111 - Bacillus anthracis virulence plasmid pXO1 C;Species: Bacillus anthracis C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           587 MNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI
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A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAB41263.1
R;Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.
Mol. Biochem. Parasitol. 42, 241-246, 1990
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry protein. Multiple of R;Reference number: A45521; MUD:91101660; PMID:2270106
A;Accession: A45521
A;Accession: A45521
A;Residues: 2260-2401 okes>
A;Residues: 2260-2401 okes>
A;Cross-references: GB:M34281
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                                                                                                                                   Query Match 5.0%; Score 187.5; DB 2; Best Local Similarity 21.7%; Pred. No. 0.29; Matches 182; Conservative 118; Mismatches 317;
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RESULT

gene from Plas parasite (Plasmodium falciparum) 1310 1200 1020 1076 47; 168 965 Major merozoite surface antigen precursor - malaria parasite (Plasmodium fall NyAlternate names: gp195 surface antigen C)Species: plasmodium fallosoite surface antigen C)Species: plasmodium fallosoite surface antigen C)Bute: 12-Feb-1993 #text_change 09-Jun-2000 C; Accession: 805603; 804650 R; Myler, P.J.
R; Myler, P.J.
A; Reference number: 805603
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A; Recession: 805603
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Ajritor Acids Res. 17, 5401, 1989

Ajritor and deduced amino acid sequence of the gpl.
Ajreference number: \$04850

Ajrocession: \$04850

Ajrocession: \$04850

Ajrocide type: mRNA

Ajross-references: EMBL:X15063

Cj.Superfamily: major merozoite surface antigen
Cj.Superfamily: major merozoite surface antigen
Fil-19/Domain: signal sequence #status predicted <SIG>
Fj.20-1639/Product: major merozoite surface antigen Indels ENILSLGKNKNIYQELIGQKSSE-NF------Query Match
4.9%; Score 185.5; DB 2;
Best Local Similarity 20.5%; Pred. No. 0.21;
Matches 170; Conservative 138; Mismatches 256; 1077 İ-----1411 셤

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Page 5

Oy 577 VLDKIKLNAXMN1LIRDKRFHYDRNNIAVG-ADESVVKEAHREVINSSTEGLL 628	Db 858 ANIYNILKLINKIKKIIDKVKEYTSEIEKNKKNINDELNNSEK 899
	426DFSSTPITMAYNQFLELEKTKQLRLDTDQVYGN 45
KILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTF	900 VIKKIEGDLSLKECRSKINSTLDDKDIDECIKNINVLKKNILNEETNITNHFKNAEETVNK
Db 1525 INISQHQCVXKQCPQNSGCFRHIDEREECKCLIMYKQEGDKC- 1566	CY 459 IATINFENGRYKVUIGSNWESVLPQIQEITAKIIENGALLMAVARSUFALAANNESUFALAAN OLO 111 (1.1. 1.1. 1.1. 1.1. 1.1. 1.1. 1.1
687 LYISNPNYKVNVYAVIKENTIINPSENGDTSTNGIKKI 724	590 IVLENKINIEMPENKALOITELKANNOINEHEINIKAEN-SINCKANNOITELE 519 POMTLKEALKIAFGFNEFNGNLQYÇGKDITEFDFNFDQQTSQNIKNOLAE
DD 1567VENPNPTCNENNGGCDADAKCTEEDSGSNG-KKI 1599	DD 1011 ADQNKKAIQKNKELFEQYKEEVTVLLNKYYAVELKNKFD-KTKNDSKQIIKE 1061
RESULT 8	QY 569 LNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVIN- 621
optry protein - Plasmodium yoelii Speries: Plasmodium voelii	VANNDKSNKA
Option 1. recommendation for the property of t	Щ
Accession: 1200//, C1001/ Keen, J., Sinhah, K., Brown, K., Holder, A. J. Biochem Baranie, C. 171 177 1004	Db 1122 NEIRTKSDDCLKETNDLEKQISNLSIDTQETKLTENGKQLKTLEELLESLK 1172
A; Title: A gene coding for a high molecular mass rhoptry protein of Plasmodium yoelii. A; Reference number: Z20508; MUID:95021522; PMID:7935623	670 QDGKTFIDFKKYNDKIPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
Accession: T28677 Status: preliminary; translated from GB/EMBL/DDBJ	Db 1173 KQKKNIEDQKKELDEVNSKIKNIENTVNQHKKNYEIGIVEKINEIAKTNKNQIESTKE 1230
Molecule type: DNA Residies 1-2269 < KRE.	Qy 721 IKK 723
Cross-references: EMBL:L27838; NID:g457145; PID:g457146; PIDN:AAA21304.1; Keen, J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.	Db 1231 LIK 1233
ol. Biochem. Parasitol. 42, 241-246, 1990 Title: Identification of the gene for a Plasmodium voelii rhontry protein Multiple of	E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-E-
1	B64635
Accession: C:5521 ;Status: preliminary	CAND-LIKE ONCEI MEMBIANE PIOCEIN HFUSZZ - RELICODACCEI PYLOII (SUIAIN 20035)
Molecule type: DNA Residues: 2131-2269 <ke2></ke2>	C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999 C;Accession: B64635
;Cross-references: GB:M34283	R, Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn
9%; Score 185; DB 2; Length 2269; 1%; Pred. No. 0.36;	son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
Matches 161; Conservative 140; Mismatches 328; Indels 214; Gaps	A.Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A.Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
1 EVKÇENKLLNESESSSĞĞLLĞYYFSDLNFQAFWVYISSTIĞDLSI PSSELENI PSE	A.Reference number: A64520; MUID:97394467; PMID:9252185 A.Accesaion: B64635
4. 8	A;Status: preliminary; nucleic acid sequence not snown; translation not snown A;Molecule type: DNA
57 NOYFQSAIWSGFIKVKKSDEYTFATSADNHVIWWVDDQEVINKASNSNKIRLEK	A,Residues: 1-2529 <tom> A;Cross-references: GB:AE000602; GB:AE000511; NID:g2314060; PIDN:AAD07969.1; PID:g23140</tom>
544 NITHINEELSKIEIKIHAS-IKNISEELEKEIGINIESLINIKVEEKKENVINLIKIEK	Query Match 4.9%; Score 184.5; DB 2; Length 2529;
QY III GKLYQIKIQYQKENPTEKGLDFKLWTDSQNKKEVISSDNLQ 152 bb 602 ikhydelesenesenesenesenesenesenesenesenesenes	Best Local Similarity 21.0%; Pred. No. 0.44; Matches 158; Conservative 94; Mismatches 261; Indels 241; Gaps 36;
153 - I.PEI.KOKSANSPKKESTSADPIVDPRINDI PINGI FIVERYTVIVKEKERTEI.SDØI SVITH	QY 123 ENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDR 178
653 YVSEMKRQINKLEKVSNTBISNDNVEGIKKKKQQIIVTKID	Db 729 ONPPAESVWSGVYWLONKTYSNKGTYYIDPNLSGQSGQSGNTLSTYTANLF 779
QY 212 EKKGLTKXKSSPEKWSTASDPYSDFEKVTGRIDKAVSPEARHPL 255	QY 179 DNDGIPDSLEVEGYTVDVKNKRFFLSPMISNIHEKKGLTKYK 220 DN 780CPSFRVNIONCHITCHNYFRONGENGERGEGYTHGHEGABLYHTWF 832
Db 693 KKKNIYEEINKLLSEISKIEKDNTSLEKVKDINLSYGQNLGNLFLEGIDEE-KKKAENTI 751	יייייייייייייייייייייייייייייייייייייי
QY 256 VAAYPIVHVDMENIILSKNEDQSTQNTDSETRIISKNTSTSRTHTSEVHGNAEVHA 311	DD 833 KTGEGVSNSDGGGANITFKASDNITMDGLNYNYDAETVYKMIQTGASQHSYATFDALN 889
Db 752 KSMEAYID-DLDNİKKKSQEIETEMDIKMDINKEMEALKISHDDDKKCHDKSKNHKENIS 910	263
312 SFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADTARLNANIRYVNTGT	890 NISVINSSESDMIWGKFSFSAKNISFSSASFS
811 DIYDKSSKIIQDFSR-ESDINDIKNKLQKNVSESQNHNSDINQCLNEV	NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPI
QY 372 APIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIALNAQK 425	Db 922 GFTNPGGSSVISANATNSLSFINSRLNGGAVYNLQANSLIFN-NTQAVFNVLY 973

OY 184 PDSLEVEGYT		Oy 550 FDFNFDQQTSQNIKNQ-LAELNATVIYTVLDKIKLNAKMNILIRDKRFHYDRNNI 603 12 SESNVANSNSTNTQNQETPETNESQNAVLIGKARNANGSLNQALDVSAKKVKIGYWHINE 781 CY 604 AVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTGLKEVINDR 659 1	RESULT 11 Tillor filamentous hemagglutinin 1 - Haemophilus ducreyi C;Species: Haemophilus ducreyi C;Species: Haemophilus ducreyi C;Species: A2-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: Tillo2 C;Accession: Tillo2 C;Accession: Tillo3 A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein. A;Reference number: Z20984; MulD:9930326; PMID:9811662 A;Accession: Tillo2 A;Accession: Tillo3 A;Accession: Tillo3 A;Accession: Tillo3 A;Accession: Tillo3 A;Accession: Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Coss. Tillo3 A;Goss.	Query Match Best Local Similarity 22.2%; Pred. No. 1.1; Batches 187; Conservative 118; Mismatches 321; Indels 218; Gaps 45; Qy 10 NESESSQGLLGYYFSDLNFQ-APMVYTSSTTGDLSIPSSELENIPSENQYF 60 162 SRTESTSQ-LVGKLHANIOLQKEAKLILNQVTGDHESNIQGALEVAGKKADLIIVN 216 Qy 61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLY 114
Qy 379PTTSLVLGKNGTLATIKAKENQLSQILAPNNYYPSKNLAPIALNAQKDFS 428 Db 974 SRGTSNFNATTQLIGNINFTLSSQSLINFNDTTLQNNANITLGNKSQAFK 1025 Qy 429 STPITMNYNQFLELEKTKQLRLDTDQVYGNIAFNFENGRVRVDTGSNWSEVLPQIQETT 488 ::: ::	126 ADFGGNTIIDTASFHFDSASSINFUNLTANGAINFNGYTFSLTKALMSVSGGFVLGNNGD 569 INATNIYTULDKIKLNAKMNILIRBKRF	Oy 695 KVNVYAVTKENTIINPSENGDISTNGIKKIL 725 Db 1360 KTLIGILSQNSATIKEMIESNQLDNITN-INEVL 1392 RESULT 10 E90598 membrane nuclease, lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Bocies: Wycoplasma pulmonis C;Bocies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: E90598 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Accession: E90598	A Status: preliminary A Molecule Pype: DNA A Molecule Vype: DNA A Molecule	Db 169 VILHNKLDLVGLTEITHBUGVKTIINELNKSSSDKWNYIVSLKKRGTTGSSGÖEEHVGII 228 Qy 98 NKASNSNKIRLEKGRLYQIKIQYQRENPTEKGL

SADNVNVKSENLALENASMSANSLDVIVTKIEVNRS----SKVSAGTANIKASNITLDG 480 448 702 -----RIAAVNPSDPLETTKPDMTL-KEALKIAFG---FNEPNGNLQYQGKDITEF 550 703 TVKNDGKLVSIENLNISSKTDFTNNGTLLGLEALKIASGGNFTNASNGSLA-SNKSLDIY 761 762 GNNFTNNGTIESVKS----LNITNNYTFINNATIKSYGVLNITSQG-NFTNDSNGTVMSH 816 D-ESVVKEAHREVINSST----EGLLL----NIDKDIRKILSGYIVEIEDTEGLKEVIND 658 | :: :|: :| :| :| :| CLINITSQAN--IINKNLLAGGGGLNLTAKGNITNDSNSTAIAVLHSNNDIN----LNA 869 RYDMLNISSL-RQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS 717 870 NNKVYNIGEIXSQAGNISVEAKLIHNDVKL-----SGNITTTK-----SGNATVK 915 :: | | | : | | | CTSR---TSDTPAI-SADSAGSMYGSNIKFVVTDKGAGVKHKGIIFSENDINIKMDGGNA 377 SLSLAGERTW-----ABTMGLNTADTARLN-----ANIRYVN---T 369 GTAPIYNVLPTTSLVLGK------NQTLA-----TIKAKENQ-LSQILAPNN-- 409 RLDTDQVYGNI ---ATYNFEN-GRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVER- 503 DENF-DOQISONIKNOLAELNATNIYTVLDK--IKLNAKMILIRDKRFHYDRNNIAVGA 607 NSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVD----VKNKRTFLSPWISNIHEKKGLT 217 KYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQ 277 SLKELYAK------KDIDILAKDIELTEKGOLOANNKIILNSTGKINLRNASEV 425 STONTDSETRIIS-KNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDH 336 GEA-----SLVAEKLDINAIDKITNNGTIAGLTANITTKALENRDNALILAHQNIN 591 QIKIQY---QRENPTEKGLDFKLYWTDSQNKKEVISSD------NLQLPELKQKSS -----YY-----PSKNLAPIALNAOKDFSS------TPITMNYNOFLELEKTKQL -----LHGNVTLNAKGNFTNSGNLTTMKELNISNIESFI----NAGNLTTGKNLEVHSNT : | : |: |: PNGITENGVKTINTDRFVVSTS-TNSI 919 TNGI 721 718 217 551 504 265 162 322 218 378 426 337 370 541 410 449 652 278 481 원 장 g à g ò 음 g ద δ 8 8 8 8 d 6 6 6 6 6

hypothetical protein ebhA [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Accession: B8921
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;
Ma, A.; Mizutani-Ui, Y.; Xobayashi, N.; Sawano, T.; Inoue, R.; Katto, C.; Sekimizu, B.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: B8921
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-6713 <AKUR>
A;Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149

Clostridium botulinum (stra

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botulinum neurotoxin type A, nontoxic/nonhemagglutinating - Clostridium C; Species: Clostridium botulinum A; Variaty: strain NIH C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 02-Jun C; Accession: S68218; S74301 R; Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma,

3097

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TVNQVKTKAEQLDQAMERLINGIQDKDQVKQSVNFTDADPEKQTAYNNAVTAAENIINQA 2942 AQKGAVTGNINQAHTVAEVT--QAIQTAQELNTAMGNLKNSLNDKDTTLGSQNFADADPE 3049 LATAKQQAKDALRQMTHLSDAQKQS-----ITGQIDSATQVTGVQSVKDNATNLDNA 2771 2772 MNOLRNSIANKDEVKASOPYVDADTDKONA----YNTAVTSAENIINATS-----OPTLD 2822 -ATIKAKENQL-----SQILAPNNYYPSKNLAPIA--LNAQKDFSSTPITMNYN-Q 438 119 QYQRENPTEKGL--DFKLYWTDSQNKKEVISSDNLQLPE---LKQKSSNSRKKRSTSAGP 173 : : | | | : : | | | | BSAVTQAANQVNTNKTALNGAQNLANKKQETTANINRLSHLNNAQKQDLNTQVTNAPNIS KKNAYNEAVRNAENILNKSTGTNV----PKDQVEAAMN-----QVNTTKAALNGTQN NG----TNANQSQVEAALSTVTTTKQALNG-----DRKVTDAKNNANQTLSTLDNLNN -----TKPDMTLKEALKIAFGFNEPNGNLQ--YQGKDITEFDFNFD--------QQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADES FLELEKTKOLRL-----YGNIAT----YNFE VVKEAHREVINSSTEGL - LLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISS-IWSGFIKVKKSDEY----TFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKI TRII---SKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSA-----GFSNSNSSTVAIDHS TVPDRDNDGIPDSLEVEGYTVDVXNKRTFLSPWISNIHEK------KGLTKYKSSPEK WSTASDPYSDFEXVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE L----SLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTL-INESESSSOCILGYYFSDINFOAPWVTS----STTGDLSIPSSELENIPSENQYFQSA I-ANKDOTKASENYIDADPTKKTAFDNAIT---QAESYLNKDHGTNKDK-----QAVEQ 2673 QGAYTDAYNAAKNIVNG-SPNVITNAADVTAATQRV-------NNAETSLNGDTN Gaps ---LRQ----DGKTFIDFKKYNDKLPLYISNPNYKVNVY--AVTKENTIINPSBN 713 NGRVRVDTGSNWSEVLPQIQE-TTARIIFNGKDLNLVERRI--AAVNPSDPLET-234; Length 6713; Query Match
4.8%; Score 182; DB 2; Length 671
Best Local Similarity 20.5%; Pred. No. 2.5;
Matches 171; Conservative 130; Mismatches 299; Indels source: strain N315 A;Experimental s C;Genetics: A;Gene: ebhA σ 2527 174 2629 226 2720 338 2823 439 466 2943 2992 3050 611 999 64 286 392 517 D. 셤 g 8 6 8 8 8 9 8 9 8 8 8 ઠે g · & à g ò 셤 8 ద ò 원 상

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FEBS Lett. 376, 41-44, 1995 A.Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components A, Accession: S6798; MUID: 96096783; PMID: 8521962 A, Accession: S68218 A, Molecule type: DNA A, Residues: 1-1193 <fuj>A, Cross-references: EMBL: D67030; NID: 92160224; PIDN: BAA11050.1; PID: d1011710; PID: 911324 A, Experimental source: strain NIH A, Accession: S74301 A, Molecule type: protein A, Residues: 1-13;45-155 <fuj>A, Experimental source: strain NIH C, Genetics:</fuj></fuj>	QY 599DRNNIAVGADESVV-KEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLK 653
A.Gene: ant C.Superfamily: tetanus toxin C.Keywords: neurotoxin F;1-1193/Product: botulinum neurotoxin type A, nontoxic/nonhemagglutinating #status expe	ace-located (import
Query Match Best Local Similarity 19.6%; Pred. No. 0.25; Matches 181; Conservative 131; Mismatches 319; Indels 294; Gaps 46;	C.Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C.Accession: C9703 R.MOIling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee R.MOILING, M. J. Sepnett. G.N.; Koonin, B.V.; Maith, D.R.
QY 42 DLSIPSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVT 88	ve Ana 325; Pi
Qy 89 MWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDF 132 : :	0000
Qy 133 KLYW 148	s: Clostridium acetobutylicum ATCC824
Qy 149DNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGY 192 Db 421 DGLKSTVDDFYSNYKIPYNRAYEYHFNNSNDSSLDNVNIGVIDNIPEIIDVNPY 474	Query Match Best Local Similarity 18.9%; Pred. No. 0.29; Matches 166; Conservative 136; Mismatches 288; Indels 288; Gaps 44;
QY 193 TVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVTG 241	OY 37 SSTIGDLSIPSSELENIPSENQYFQSAIW-SGFIKVKKSDEYTFATSADNHVTWWVDDQE 95
OY 242 RIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTQNTDSETRIISKUTST 295	OY 96 V-INKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVI 146
Qy 296 SRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNS-STVAIDHSLSLAGERT 345 Db 572 DITATQEINTNCGINKVVTWFGKALNILNTSDSFVEEFQNLGAISLINKKENLSMPIES 631	Qy 147 SSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVBGYTVDVKNKRT 201
Qy 346 WAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQT 390 : :	Qy 202 FLSPWISNI
OY 391 LATIKAKENQLSQILAPINYYPSKNLAPIALNAQKDFSS-TPITMN 435	CY 221 SSPEKWSTASDPYSDFEKVTGRIDKOVSPEARHPLVAA 258 :
QY 436YNOPLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQ 483 Db 752 AAICVFESNIYPKFISFMEQCINNINIKTKEF1QKCTNINEDEKLQL 798	Qy 259 YPIVHVDMENIILSKNEDQS-TQNTDSETRIISK-NTSTSRTHTSEVHGNAEVHASFFDI 316
OY 484 IQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDWTLKEALKIAPGFNEPNGN 539	Qy 317 GGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANI 364
Oy S40LQYQGKDI-TEFDFNFDQQTSQNIKNQLAELNATNIYTV 577 B50 VIGDASGKNTSIEY-SKDIGLVYGINSDALYLNGSNQSISFSNDFFENGLTNSFSIYFWL 908	Qy 365 -RYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYY 411
QY 578LDKIKLNAKM	Qy 412 PSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQV 455 :

305 GNAEVHASFPDIGGSVSAGPSNSNSTVAIDHSLSLAGERTWAETMGLNTADTARLNA 655 TNQSNSSEATKVDNNSSTHSSNILNSGSNDSSDSDSDSDSDSSNL 363 NIRYWYGTAPIYNVLPTTSLVLGRNQTLATIKAKENQLSQILAPNNYYDSKNLAP 700SSSPNLETNQTIASTKSKPSEVNNLSENPKKYSSSNSVQENSTDHE 719 IALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGS 71	Qy 476 NWSEVLPQIQETTARIIFNGKDLNLVERRIAANNPSDPLETTKPDMT 522	Qy 638 ILSGYIVELEDTEGLKEV Db 969EVETWEDSKTV Qy 689 ISNPNYKVNVYAVTKENT Db 1020	Search Completed: May 3, 2004, 19:41:13			
9y 456YGNIATYNFENGRVRYDTGSNWSEVLPQIQETTARI-IFNGKDLNLVERRIAAVNP 510 bb 485 INSGIGNIDDYSKLQTEAVDASKLEAVNDDIKKIKADKGRDLTIQEIRDSVKKT 538 cy 511 SDPLETTKPDMTLKEALKIAF-GFNEPNGNLQYQGKDLTBFDFNFDQQTSQNIK 563	600 RNNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKLISGYIVE	RESULT 15 A86827 hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C.Species Lactococcus lactis subsp. lactis C.Species Lactococcus lactis subsp. lactis C.Species 13-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C.Accession: A86827 R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli	Genome Kas: 11, 731-732, ZUU1 Genome Seguence of the lactic acid bacterium Lactococcus lactis se A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Reference reliminary A;Molecule type: DNA A;Residues: 1-1072 <sto> A;Crose-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146 A;Experimental source: strain IL1403 C;Genetics: A;Gene: yqfG</sto>	Query Match 4.7%; Score 178.5; DB 2; Length 1072; Best Local Similarity 19.4%; Pred. No. 0.25; Matches 160; Conservative 142; Mismatches 342; Indels 179; Gaps 30; Qy 2 VKQENRILNESESSSQGLLOYYFSDINFQAPMVVTSSTTGDLSIPSSELEN	QY 53IPSENQYPQSAIMGGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKI 106 100 EISYDSENSYSLSSSNQINSNSRKEKDSNQSSLGSSMSSNEESEHSNSNINETNNSSEI 419 QY 107 RIEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELK 157 DD 420 TNILPPSNPTESNSVSDQTSSEASTNSNSSISLSPSNISSTSDSESATNSSDFSNVAEVA 479	Qy 158 QKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEK 213 Db 480 NNSLASVNNSSSSVLSSTSTADNLGINQSGSDNLTKDSSEISTSGAFLSSNQTSS 534 Qy 214 KGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPBARHPIVAAYPI 261 Db 535 EASTNSNSSISLSPSNISSTSVLESTTSSSNFSNVAEVANNSLASVNNSSSSVLSSTSTA 594 Qy 262 VHVDMBNIILSKNBDQSTQNTDSETRTISKNTSTSRTTSEVH 304 Db 595 DNLEINQFGSDNLTKDSSEISTSGAFLSSNQTSSBASSNSMSSINSPSLSLSTSNSFS 654

OM protein - protein search, using sw model

May 3, 2004, 19:27:02 ; Search time 8.2539 Seconds (without alignments) 4636.784 Million cell updates/sec Run on:

US-09-848-909A-8 3773 1 EVKQENRLINESESSSQGLL......TSTNGIKKILIFSKKGYEIG 735

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	3 bacillus an	2 bacillus an	2 plasmodium				1 schizosacch			8 mycoplasma							1 schizosacch	4 saccharomyc	9 plasmodium		_					helic					7 caenorha		0
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* 2	Match			4.9	4.9	4.6	4.5	4.5	4.4	4.3	4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.1		4.1		4.1	4.1	4.1	4.1	4.1	4.1	4.0	4.0	4.0	•	3.9	•	•
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1255 1225 1225 1466 1726 2376 1091 1162 1397 2339	
148 147 147 146 146 146 146 146 146 146 146 146 146	
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### ALIGNMENTS

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MEDLINE=94131936; PubMed=8300513;
Koehler T.M., Dai Z., Kaufman-Yarbray M.;
Regallation of the Bacillus anthracis protective antigen gene: CO2 and a trans-acting element activate transcription from one of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=21125576; PubMed=11222612;
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"Involvement of domain 3 in oligomerization by the protective antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Sterne;
MEDLINE=55050722; PubMed=7961869;
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The chymotrypsin-sensitive site, FPD315, in anthrax toxin protective antigen is required for translocation of lethal factor.";
J. Biol. Chem. 269:29039-29046(1994).
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MEDLINE=21438996; PubMed=11554763;
Ahrlja N., Kumar P., Bharnagar R.;
Ahrlja N., Kumar P., Bharnagar R.;
"Hydrophobic residues Phe52, Phe554, Ile562, Leu566, and Ile574 are
required for oligomerization of anthrax protective antigen.";
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"Protocolytic activation of receptor-bound anthrax protective antigen on macrophages promotes its internalization.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Varughese M., Teixeira A.V., Liu S., Leppla S.H.; defication of a receptor-binding region within domain 4 of the protective antigen component of anthrax toxin."; Infect. Immun. 67:1860-1865(1999).
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                                                                                         Milne J.C., Furlong D., Hanna P.C., Wall J.S., Collier R.J.;
"Anthrax protective antigen forms oligomers during intoxication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [12]
MUTAGENESIS OF PHE-581; PHE-583; ILE-591; LEU-595 AND ILE-603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21255689; PubMed=11356563;
Khanna H., Chopra A.P., Arora N., Chaudhry A., Singh Y.;
RROle of residues constituting the 2beta1 strand of domain
biological activity of anthrax protective antigen.";
FEMS Microbiol. Lett. 199:27-31(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Sterne; WEDLINE3102804; PubMed=11178978; WEDLINE=21092804; PubMed=11178978; Batra S., Gupta P., Chauhan V., Singh A., Bhatnagar R.; Trp 346 and Leu 352 residues in protective antigen are the expression of anthrax lethal toxin activity."; Biochem. Biophys. Res. Commun. 281:186-192(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUTAGENESIS OF GLN-512; ASP-541; LEU-543 AND ARG-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                        [9]
MUTAGENESIS OF PHE-342; PHE-343 AND ASP-344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF TRP-375; MET-379 AND LEU-381.
 266:15493-15497(1991).
                                                                                                                                             Biol. Chem. 269:20607-20612(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sterne;
MEDLINE=99185012; PubMed=10085028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           moiety of anthrax toxin.";
J. Bacteriol. 183:2111-2116(2001)
[15]
                                                                       MEDLINE=94327640; PubMed=8051159;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriol. 176:586-595(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS OF DOMAIN 4 LOOPS.
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                                                                                                                              mammalian cells.";
                                      CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                            POXIN REGULATION
                                                                                                                                                                                    CHARACTERIZATION
 Chem.
 Biol.
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recognition.

PTM: Proteolytic activation by furin or a furin-like protease cleaves the protein in two parts, PA-20 and PA-63; the latter is the mature protein. The cleaves of parts, ball of the cell surface and probably in the serum of infected animals as well; both native and cleaved PA are able to bind to the cell receptor. The release of PA-0 from the remaining receptor-bound PA63 exposes the binding site for EF and LE, and promotes oligomerization and internalization of the protein.

MISCELLANDOUS: In Ref. 9 multiple mutagenesis experiments were performed that showed that the residues present in the small loop of domain 4, and not the ones in the large loop, are involved in
                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
MEDLINE=97192099; Pubmed=9039918;
Petosa C., Collier R.J., Klimpel K.R., Leppla S.H., Liddington R.C.;
Crystal structure of the anthrax toxin protective antigen.";
Nature 385:833-838(1997).
                                                                         MUTAGENESIS OF PRO-213; LEU-216; PHE-231; LEU-232; PRO-234; ILE-236;
ILE-239; TRP-255 AND PHE-265.
                                                                                                                                 anthrax protective antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor recognition.
SIMILARITY: BELONGS TO THE BACTERIAL BINARY TOXIN FAMILY
                    Sellman B.R., Nassi S., Collier R.J.,
"Point mutations in anthrax protective antigen that block
ASP-454 AND PHE-456
                                                                                                                       Chauhan V., Bhatnagar R.;
"Identification of amino acid residues of involved in binding with lethal factor.";
Infect. Immun. 70:4477-4484 (2002).
                                                     Biol. Chem. 276:8371-8376(2001)
                                                                                                             MEDLINE=22112896; PubMed=12117959;
                                                                                                                                                                                                                                                         MEDLINE=21428689; PubMed=11544370;
 MUTAGENESIS OF LYS-426; ASP-454 AM
MEDLINE=21269403; PubMed=11113126
                                                                                                                                                                                                                                                                   Mock M., Fouet A.; "Anthrax.";
                                                                                                 STRAIN=Sterne;
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540 360 449 480 720 749 420 569 600 629 99 300 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 389 QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180 240 ω Ω DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL NNIAVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYIVEIEDTEGLKEVINDRY EVKQENRLIANESESSSQGLLGYYFSDINFQAPMVTSSTTGDLSIPSSELENIPSENQYF DGI PDSLEVEGYTVDVKNKRTFLSPWI SNI HEKKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 270 GRIDKOVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSQTRTISKNTSTSRTHT 301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNIGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR 1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF ö Length 764; Indels Score 3764; DB 1; Pred. No. 4.1e-178; 1; Mismatches 1; IKKILIFSKKGYEIG 735 99.8%; larity 99.7%; Conservative 1 IKKILIFSKKGYEIG Similarity Best Local Simi Matches 733; 721 450 9 361 390 481 601 210 241 421 61 90 121 150 181 Query Match g ò 셤  $\delta$ g ò g ò g à g à g δ qq 셤 ò g g ò g ò  $\delta$  $\delta$ 

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MEDLINE-89172073; PubMed=3148491; Welkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Leppla S.H. Schmidt J.J.; Lowe and analysis of the DNA encoding protective antigen of "Sequence and analysis of the DNA encoding protective antigen of

Bacillus anthracis."; Gene 69:287-300(1988) SEQUENCE FROM N.A. 9 646

23; Gaps

Length 204;

CRC64;

204 AA; 23029 MW; E1657B23AE4273FD

SEQUENCE Query Match

Local Matches

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CONFLICT

T -> A (IN REF. 1).
KSCNCILIYVEVSQLMNSVFY -> NHVIVYLSM

182 93 204

Transmembrane. POTENTIAL

EMBL; M22589; AAA22636.1; -EMBL; AF065404; AAD32415.1; -PIR; G59104; G59104.
PIR; 139933; 139933.
HSSP; P13423; 1ACC.
Hypothetical protein; Plasmid; Tr
TRANSTEM 162 93 93 T ->
CONFLICT 93

9

647 EDTE------GLKEVINDRYDMLNISSLRODGKTFIDFKKYNDKLPLYISNPN 693 

694 YKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKGYEI 734

587 MUILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI 

al Similarity 34.6%; Pred. No. 2.5e-05; al Similarity 34.6%; Pred. No. 2.5e-05; 56; Conservative 36; Mismatches 47; Indels

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MSP1_PLAFK

ID MSP1_PLAFK

ID MSP1_PLAFK

ID MSP1_PLAFK

AC P04932;

DT 13-AUG-1987 (Rel. 05, Created)

DT 01-FB2-1996 (Rel. 34, Last sequence update)

DT 01-FB2-1996 (Rel. 34, Last annotation update)

DT 01-C7-1996 (Rel. 34, Last annotation update)

DE Merozoite surface protein 1 precursor (Merozoite surface antigens)

DE MSP-1.

OS Plasmodium falciparum (isolate K1 / Thailand).

C Eukaryota; Alveelata; Apicomplexa; Haemosporida; Plasmodium.

OX CB1_TAXID=5839;

RN 11

RP SEQUENCE FROM N.A.

RM MEDLINE=86136024; Pubmed=3004972;

RA MEDLINE=86136024; Pubmed=3004972;

RA MACKAY M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,

RA Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U.,
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Bacillus

Bacillaceae;

Bacteria; Firmicutes; Bacillales; NCBL_TaxID=1392;

N.A.

FROM

[1] SEQUENCE ?

PXO1-111. Bacillus anthracis. Plasmid pXO1.

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YPB1_BACAN STANDARD; PRT; 204 AA. P13422; Q9X377; Corated) 10-Opn-1990 (Rel. 13, Created) 16-OCT-2001 (Rel. 40, Last sequence update) Hypothetical protein pX01-111.

RESULT 2 YPB1_BACAN

REVISIONS, SEQUENCE FROM N.A.

Bab W., TOOLle R., Bujard H.;
Submitted (JWN-1995) to the EMBL/GenBank/DDBJ databases.

-i- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor [2] REVISIONS, 

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> kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont. 83 kDa, :- PTM: Merozoite surface antigen contain the sequence of

(Potential)

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InterPro; IPR006209; EGF_like. Pfam; PF00008; EGF; 1. Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;

GPI-anchor Transmembrane; SIGNAL

à

DB 1; Length 1630; Indels ,256; 0.12; Conservative 138; Mismatches 4.9%; Score 185.5; 20.5%; Pred. No. 0.1 Best Local Similarity Matches 170; Conserv Query Match

47;

1191 1012 KKKTVGKYKMQIKKLTLLKEQLESKL--NSLNNPKHVL--QNFSVFNKKKBABIABTBN 1067 1095 TLSEESIQTEDNYASLENFKVLSKLEGKLKDNLNLEKKKLSYLSSGLHHLIA-----E 1147 T-----KGLVKYYNGESSPLK 1094 957 SFTNFVKSKADD----INSLNDESKRKKLEEDINKLKKTLQLSFDLYNKYKLKLERLFD 1011 223 265 ENILSLGKNKNIYQELIGQKSSE-NF-------YEKILKDSDTFYNE 956 -----QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS 168 63 TSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKY---KSSP-----EKWSTASDPYSDFE-----KVTGRIDKNVSPEAR-----HPLVAAYPIVHVD MENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS LKEVIKNKN---YTGNSPSENNT-------DVNNALESYKKFLPEGTDVATVVS 5 ENRL-LNESESSSOGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA 64 IWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNS------NKIRLEKGRLY-169 918 115 1068 224 g 셤 ò 셤 ò ò 셤  $\stackrel{>}{\circ}$ QC Op 8

1456 1401 576 628 1192 ESGSDTLEQSQPKKPASTHVGAES---NTITTSQ-NVDDEVDDVIIVPIFGESEEDYDDL -----QFLELEKTKQLKLDTDQV-YGNIAT-----YNFENGRVRVDTGSNWSEVL PQIQETTARIIFNGKDLNLVERRIAAVNPSDPL-----ETTKPDM-TLKEALKIAFGF 534 NEPN----GNLQYQGXDITE------FDFNFDQQTSQNIKNQLAELNATNIYT LNIDKD--IRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLP 1516 LNISQHQCVKK------QCPQNSGCFRHLDE------REECKCLLNYKQEGDKC-NSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTT-----SLVLGKNOTLATIKAKENOLSOILAPNNYYPSKNLAPIA---LNAQKDFSSTPITMNYN 577 VLDKIKLINAKMN--ILIRDKRFHYDRNN-----IAVG-ADESVVKEAHREVINSSTEGLL 687 LYISNPNYKVNVYAVTKENTIINPSBNG------DTSTNGIKKI 438 482 1402 629 1558 a g  $\delta$ g

01-FEB-1996 (Rel. 33, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Merozoite surface protein 1 precursor (Merozoite surface antigens) 13-AUG-1987 (Rel. 05, Created) STANDARD; (PMMSA) (P195) PLAFW RESULT 4 P04933

MEDLINE=86014355; PubMed=2895820; Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno V., Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T., Plasmodium falciparum (isolate Wellcome). Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBL_TaxID=5848; SEQUENCE FROM N.A. Freeman R.R.;

. <del>6</del> PTM: Merozoite surface antigen contain the sequence of 83 kDa, kDa and 19 kDa antigens which are the major surface antigens of merozoites. The maturation take place during schizont. Holder A.A.; Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases. -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985). (Potential) REVISIONS 

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1076 T-----KGLVKYYNGESSPLK 1103 LKEVIKNKA---YTGNSPSENNT------DVNNALESYKKFLPEGTDVATVVS 1200 965 ---EKWSTASDPYSDFE-----KVTGRIDKNVSPEAR------HPLVAAYPIVHVD 265 MENIILSKNEDOSTQNTDSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS 325 NSNSSTVAIDHSLSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTT---- 381 -----QFLELEKTKQLRLDTDQV-YGNIAT-----YNFENGRVRVDTGSNWSEVL 481 64 IWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNS------NKIRLEKGRLY-966 SFINFVKSKADD-----INSLNDESKRKKLEBDINKLKKTLQLSFDLYNKYKLKLERLFD 5 ENRI-LNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSA -----YEKILKDSDTFYNE ----QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRS 1021 KKKTVGKYKMQIKKLTLLKEQLESKL--NSLNNPKHVL--QNFSVFFNKKKEAEIAETEN TSAGPTVPDRDNDG1PDSLEVEGYTVDVKNKRTFLSPW1SNIHEKKGLTKY---KSSP---SLVLGKNOTLATIKAKENQLSQILAPNNYYPSKNLAPIA---LNAQKDFSSTPITMNYN PQIQETTARIIFNGKDLNLVERRIAAVNPSDPL-----ETTKPDM-TLKEALKIAFGF 1370 DSID-----TDINFA------NDVLGYYKILSEKYKSDLDSIKKYINDKQGE NEPN----GNLQYQGKDITE------FDFNFDQQTSQNIKNQLAELNATNIYT Gaps GLCNAC. ) (POTENTIAL)
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(GLCNAC. ) (POTENTIAL)
(GLCNAC. ) (POTENTIAL) Indels 265; DB 1; Length 1639; Signal; Glycoprotein; MW; 2C255B6616C87F6E CRC64; Query Match
Best Local Similarity 20.5%; Pred. No. v.r.,
Matches 170; Conservative 138; Mismatches 256; ENILSLGKNKNIYQELIGQKSSE-NF------(GLCNAC PDB; 1CEJ; 28-MAY-99.
Therbro; 1RR006209; EGF like.
Pfan; PF00008; EGF; Malaria; Merozoite; Polyprotein; Repeat; POTENTIAL MEROZOITE S N-LINKED (G N-LINKED (G N-LINKED (G N-LINKED (G N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C N-LINKED (C 187618 1116 268 764 764 883 920 11068 11165 11265 Æ. PIR; A24594; A24594 PIR; S05603; S05603 PDB; 1CEJ; 28-MAY-9 1639 224 266 1157 382 CHAIN CARBOHYD CARBOHYD CARBOHYD CARBOHYD 1077 1411 CARBOHYD CARBOHYD 115 169 438 CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD SEQUENCE SIGNAL  $\delta$ do a a a 유 g g ò ò ò  $\overset{\circ}{\circ}$ ઠે ò à ò

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). 1466 IQDKLADFKKNNNFVGIADLSTDYNHNNLTKFLSTGMVFENLAKTVLSNLLDGNLQG-M 1524 LNISQHQCVKK------QCPQNSGCFRHLDE------REECKCLLNYKQEGDKC- 1566 QYFQSAIWS-GFIKVKKSDE-----YTFATSADN---HVTMWVDDQEVINKASNSNK 105 145 577 VLDKIKLNAKWN--ILIRDKRFHYDRNN----IAVG-ADESVVKEAHREVINSSTEGLL 1 EVKQENRLINESES----SSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSEN ------ESQSAQESEQGSEDDFEYKMKNEKSTSEBTENTSESRDQGFAKDAYTKNKV ISSDNLQLPEL-------KQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVE LNIDKD--IRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLP · - - - YWTDSQNKKEV SEQUENCE FROM N.A.
STRAIN=S28BC / AB972;
STRAIN=S28BC / AB972;
STRAIN=S28BC / AB972;
STRAIN=S28BC / AB972;
BOWNEAN S., Churcher C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A. Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XIII."; 003661; 004988; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 10-CCT-2003 (Rel. 42, Last annotation update) Hypothetical 187.1 kDa protein in GUA1-ERG8 intergenic region. YMR219W OR YM261.13 OR YM9959.01. Saccharomyces cerevisiae (Baker's s yeast). Eukaryota; Fungi; Ascomycota, Saccharomycetiaes; Saccharomycetaes; Saccharomycetaes; --VENPNPTCN----EN-----NGGCDADAKCTEEDSGSNG-KKI 1599 4.6%; Score 175; DB 1; Length 1658; larity 18.8%; Pred. No. 0.4; Conservative 134; Mismatches 285; Indels 272; 687 LYISNPNYKVNVYAVTKENTIINPSENG------DTSTNGIKKI Hypothetical protein. SEQUENCE 1658 AA: 187137 MW; 3893F968305A757D CRC64; GO:0005634; C:nucleus; IDA. GO:0006348; P:chromatin silencing at telomere; IMP. IRLEKGRLYQIKIQYQRENPTEKGLDFKL----EMBL; Z49809; CAA89934.1; -. EMBL; Z49939; CAA90190.1; -. PIR; S55101; S55101. Germonline; 142894; -. Nature 387:90-93(1997). SGD; S0004832; ESC1. Similarity NCBI_TaxID=4932; Query Match Best Local Simi Matches 160; YEAST 1525 290 8 349 106 629 409 g g 음 ద ઠે 엄 8 셤 à ò ઠે ਨ

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                                       GYTVDVKNKRTFL---SPWISNIHE--KKGLTKYKSS----PEKWSTASD-----
                                                       ------PYSDFEKVIGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQ
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STRAIN=W303;

BDDLINE 2474309; PubMed=9335333;

Michaelis C., Closk R., Nasmyth K.;

"Cohesins: chromosomal proteins that prevent premature separation sister chromatids.";

Sister Aromatids.";

Cell 91:35-45 (1997). SMC3 YEAST STANDARD; PRT; 1230 AA.
P47037.
P47037.
P47037.
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Structural maintenance of chromosome 3 (DA-box protein SMC3).
SMC3 OR YUL074C OR U1049.
SMC3 OR YUL074C OR U1049.
Succharowyces cerevibiae (Baker's yeast).
Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces. E., Chalwatzis Boles SEGUENCE FROM N.A. MEDLINE=96208490; PubMed=8641269; Galibert F., Alexandraki D., Baur A., [1] SEQUENCE FROM N.A. 

[4] PENTIFICATION IN A COHESIN COMPLEX WITH SMC1; IRR1 AND MCD1, AND INTERACTION OF THE COHESIN COMPLEX WITH SCC2.

WEDLINE=99145468; PubMed=9990856;
A TOCH A., Closk R., Uhlamn F., Galova M., Schleiffer A., Nasmyth K.;
A TOCH A., Closk R., Uhlamn F., Galova M., Schleiffer A., Nasmyth K.;
A TOCH A., Closk R., Uhlamn F., Galova M., Schleiffer A., Nasmyth K.;
A TOCH A., Closk R. (13:320-333(1999).

R. Gares Dev. 13:320-333(1999).

R. Gares Dev. 13:320-333(1999).

R. Gares Dev. 13:320-333(1999).

R. Gares Dev. 13:320-333(1999).

R. M. [5]

PR. MEDLINE=21980168; PubMed=11983169;

R. MEDLINE=21980168; PubMed=11983169;

R. Mabline=21980168; PubMed=11983169;

R. Mabline=21980168; PubMed=11983169;

R. Mabline=21980168; PubMed=11983169;

R. Masmyth K.;

Haaring C.H., Loewe J., Hochwagen A., Nasmyth K.;

T. Monlecular architecture of SMC proteins and the yeast cohesin Chuat J.-C., Coster F., Cziepluch C., De Haan M., Domdey H.,
Durand P., Entian K.-D., Gatius M., Goffeau A., Grivall L.A.,
Herbert C.J., Heumann K., Higer F., Hollenberg C.P.,
Huang M.-E., Jacq C. Jauniaux J.-C., Katsoulou C., Kirchrath L.,
Kleine K., Kordes E., Koetter P., Liebl S., Louis E.J., Manus V.,
Mewes H.-W., Miosga T., Obermaler B., Perea J., Pohl T.M.,
Portetelle D., Pujol A., Purnelle B., Ramezani Rad M., Rasmussen S.W.,
Rose M., Rossau R., Schaaff-Gerstenschlaeger I., Smits P.H.M.,
Scarces T., Soriano N., Tovan D., Tzermia M., Van Broekhoven A.,
Vandenbol M., Wedler D.H., Von Wettstein D., Wambutt R., Zagulski M.,
Zollner A., Karpfinger-Hartl L.;
Complete nucleotide sequence of Saccharomyces cerevisiae chromosome [3]
SEQUENCE FROM N.A.
STRAIN=S288C / FY1678;
Sor F.J.; (JUN-1995) to the EMBL/GenBank/DDBJ databases. EMBO J. 15:2031-2049(1996). 

Mol. Cell 9:773-788(2002).

Mol. Cell 9:773-788(2002).

Mol. Cell 9:773-788(2002).

Mol. Cell 9:773-788(2002).

Mol. Cell 9:773-788(2002).

Somplex is required for the cohesion of sister chromatida after complex is required for the cohesion of sister chromatida after DNA replication. The cohesin complex apparently forms a large proteinaceous ring within which sister chromatids can be trapped. At anaphase, the complexes are composed and dissociates from chromatin, allowing sister chromatids to segregate.

STBUNIT: Cohesin complexes are composed of the SMC1 and SMC3 heterodimer attached via their hinge domain, MCD1/SCC1 which linke them, and IRR1/SC3, which interacts with MCD1. The cohesin complex also interacts with SCC2, which is required for its association with chromosomes.

C. SUBCELLULAR LOCATION: Nuclear protein. Associates with chromatin. Before prophase; it is scattered along chromosome arms. At anaphase, the MCD1 subunit of the cohesin complex is cleaved, ladding to the dissociation of the complex from chromosomes, allowing chromosome separation.

C. I. DOMAIN: The Itakible hinge domain, which separates the large intramolecular coiled coil regions, allows the heterotypic interaction with the corresponding domain of SMC1, forming a V-shaped heterodimer. The two heads of the heterodimer are then connected by different ends of the cleavable MCD1 protein, forming a ring structure (By similarity).

C. SIMILARITY: Belongs to the SMC family. SMC3 subfamily. complex.";

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EMBL; Y14278; CAA74655.1; -.
EMBL; Z49349; CAA89366.1; -.
EMBL; X88861; CAA61313.1; -.
BPLR; S56850; S56850.
GermOnline; 141688; -.

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                                                                                                                                                                                                                                                            59 YFQ----SAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINK--- 99
 SGD; S0003610; SMC3.

RGD; G00001515; P:sporulation (sensu Saccharomyces); IMP.

G0; G0:0001130; P:synaptonemal complex formation; IMP.

RGC; G0:0001130; P:synaptonemal complex formation; IMP.

RIGHERPO; IPR00345; SMC_C.

RIGHERPO; IPR003465; SMC_C.

R InterPro; IPR003465; SMC_C.

R Pfam; PF02463; SMC_C.

R Mitosis; Cell cycle; Chromosome partition; ATP-binding; Coiled coil;

M Mitosis; Cell cycle; Chromosome partition; ATP-binding; Coiled coil;

W Muclear protein.

R PEND 32 39 ATP (POTENTIAL).

TO DOMAIN 483 684 COILED COIL (POTENTIAL).

POMAIN 483 684 COILED COIL (POTENTIAL).

POMAIN 685 1041 COILED COIL (POTENTIAL).
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4.5%; Score 169.5; DB 1; Length 1230;
Best Local Similarity 19.8%; Pred. No. 0.5;
Matches 182; Conservative 136; Mismatches 355; Indels 247;
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COLLED COLL (POTENTIAL).
RIBXRBLE HINGE.
COLLED COLL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
141336 MW; B152D88F7780341F CRC64;
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--ISSLRODGK
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MEDLINE=20223868; PubMed=10759889;
Ding D.-Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
Hiraoka Y.;
                                                                                                                                                                                                             Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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01-0CT-1996 (Rel. 34, Created)
01-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Spornlation-specific protein 15.
SPOIS OR SPACIF3.06C.
  --VINDRYDM-
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                                                                            DT----STNGIKKILIFSK
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SEQUENCE OF 705-871 FROM N.A.
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YQGKDIT-EFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR

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                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.5%; Score 168; DB 1; Length 1957;
Best Local Similarity 20.5%; Pred. No. 1.1;
Matches 178; Conservative 132; Mismatches 327; Indels 232; Gaps
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 spore membrane
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COLLED COIL (POTENTIAL).
MW; 3F480CA06171D9DA CRC64;
FUNCTION: Has a role in the initiation of
                              -!- SUBUNIT: Monomer.
-!- SUBCELLULAR LOCATION: Spindle pole body.
-!- SIMILARITY: Belongs to the MPC70 family.
                                                                                                                                                                                             EMBL, Z70690, CAA94624.1; -.
EMBL, AB027811; BAA87115.1; -.
PIR, T38077, T38077.
GeneDB Spombe, SPACIF3.06c; -.
Sporulation; Colled coll.
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Surfalerso;
Surfalerso;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessierse P., Bolctin A., Borchert S.,
Azevedo V., Bertero M.G., Bessierse P., Bolctin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Benizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly B.J., Grandi G.,
Guiseppi G., Guy B.J., Hage K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Kasahara Y., Klaerr-Blanchard M., Klein C.,
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SEQUENCE FROM N.A.
SERAIN=168 / BGSC1A1;
MEDLINE=95219088; PubMed=7704263;
Yoshida K.T.I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
Yoshida K.T.I., Sano H., Seki S., Oda M., Fujimura Bacillus Subtilis
genome containing the hut and wapA loci.";
Microbiology 141:337-343(1995).
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creation of a 177 kb contig
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STRAIN=168 / BGSC1A1;
MEDLINE=97124196; PubMed=8969509;
Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai Miwa Y., Fujita Y.;
Sequencing of a 65 kb region of the Bacillus subtilis genome containing the lic and cel loci, and creation of a 177 kb contincovering the gnt-sacXY region.";
Microbiology 142:3113-3123(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product
gene encoding a 258 kDa precursor two-domain ligand-binding
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01-007-1994 (Rel. 30, Last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
MAPA OR N17G OR BSU39230.
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MEDLINE=93302506; PubMed=8316082;
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Mol. Microbiol. 8:299-310(1993)
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1732 1751 2-15. 1753 1772 2-16. 1795 1814 2-17. 1840 1859 2-18. 1861 1880 2-29. 1861 1906 2-21. 1908 1927 2-22. 1968 2027 2-24 (APPROXIMATE). 2008 2027 2-25. 2038 2047 2-26. 2058 2047 2-26. 2058 2047 2-26. 2058 2047 2-26. 2058 2047 2-27. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29. 2058 2047 2-29.	h Similarity 18.2%; Pred. No. 1.7; 73; Conservative 126; Mismatches 336; Indel	1 EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIP 54	55 SENQYFQSAIMSGFIKVKKSDEYTFATSADNHVTM	90wVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR 12 	23 ENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVP 177	77DRDNDG1PDSLE-VEGYTVDVKAKRTFLSPWISNIHEKKGLTKYKSSP 22	24 EK-WSTASDPYSDFEKVTGRID-KOVVSPEARHPLVAAYPIVHVDMENIILSKNE 27	76DOSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS 32: 	26 NSNSSTVAIDHSLSLAGERTWAETWGLNTADTARINANIRYUNTGTA 377 59 GKGFETLDLGNQTSWTTKGKKIWPTSAEIKAGKYALHLKDGSGAELPINPGPTYKNAGGD 71	73 PIYNVILPTTSLVIGKNQTLATIKAKENQLSQILAPNNYYPSKNLA 41	18PIALNAQKDFSSTPITWAYNQFLELEKTKQLRL 45	51 DIDQVYGN	2 - P	18KPDMTLKBALKIAFG-FNEPNGNLQYQGKDITEFDFNFDQQTSQNIXNQLAEL- 56
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1079 LKKVTDTDGTVTSYDYDSEGRLVKQYSANSTEAKPVFTEYQYSGHRLEKAINAKKETYVY 1138 GGAMYIDEDATTHRFTKKADGTYQPPTGVYLELTETADQFILKTKDQTNAYFNKKGGKLQ 1018 1019 KVVDGHNNATVYTYNDKNQLTAITDASGRKLTFTYDENGHVTSITGPKNKKVTYSYENDL 630 NIDKDI------RKILSGY-----IVEIEDTEGLKEVINDRYDMLNI 665 -----NATNIYTVLDKIKLNAKMNILIRDKRFHYDRN-570

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=97103775; PubMed=8948101;
Cataphuch C., Kordes E., Pujol A., Jauniaux J.-C.;
Sequencing analysis of a 40.2 kb fragment of yeast chromosome X reveals 19 open reading frames including URA2 (5' end), TRKI, PBS2, SPTIO, GCDI4, RPEI, PHO86, NCA3, ASFI, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon."; PUTL3 YEAST STANDARD; PRT; 1803 AA.
P47024; P881925
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transposon Ty4 207 7 Mba hypothetical protein.
TY4B OR YJL113W OR 10780.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyc RESULT STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE STATE

1 EVKQENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF Query Match
4.3%; Score 164; DB 1; Length 1803;
Best Local Similarity 19.5%; Pred. No. 1.6;
Matches 162; Conservative 123; Mismatches 274; Indels 27 ò

EMBL; Z49389; CAA89409.1; -. SGD; S0003649; YUL113W.
InterPro; IPRO01584; Rve.
InterPro; IPRO01898; Znf_CCHC.
Pfam; PF00665; rve; 1.
SMART; SM00343; ZnF_C2HC, 1.
Transposable elemenf; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;

1078 QLKKTN---HETSFPKEGSIG---TNVKFRNTNNEISLKTGDTSLPIKTLESINNHH--- 1128 EKENHHPPPIEDIVDM----SDQTDMESNCQDGNNLKELKVTDKNVPTDNGTNVSPR-- 1193 121 QREN----PTEKGLDFKLYMTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVP 176 **QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY** DRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKK--------GLTKY-----61 g ò 엄  $\dot{\delta}$ d

|| : : : : | || STARCVSSTEAELHAIYEGYADSETLKVTLKELGEGDNNDIVMITDSKPAIQGLNRSYQQ 1735 1527 RMD--KKYNEELKKIRKSSIPHMSTYK------IDPKKDVLQMSEEEFRQGVLKL 1573 274 NEDOSTONIDSETRIISKN--TSISRIHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSST 331 332 VAIDHS-----LSLAGERT-WAETMGLNTADT-ARLNANIRYVNTGTAPIYNVLP-TTSL 383 1305 VFDVDVKYSRSE---IPDNLIVPTNTIFTKKRNG---IYKARIVCRGDTOSPDTYSVITT VLGKNQTLATIKAKENQ-----LSQI-LAPNNYYP----SKNLAPIALNAQKDFS RVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNP-SDPLETTKPD-----MTL KEALKIAFGFNEPNGNLOYOGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKL 584 NAKWINILIRDKRFHYDRN----NIAVGADESVVKEAHRE----VI------NS STEGLLLNIDKDIRKILSGY---------IVEIEDT----EGLK----STPITMNYNOFL-ELEKTKOLR------LDTDQVYGNIATYNFENGRV-----1736 PKEKFTWIKTEIIKEKIKEKSIKLLKITGKGNIADLLTKPVSASDFKRF 1784 -----EVINDRYDMLNISSLRQDGKTFI------DFKKY 681 1468 1676 1194 384 429 470 524 1621 654 9 6 9 6 6 6 6 9 6 6 6 B 엄 8 g ò 8

Mycoplasma hyorhinis. Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma. NCBI_TaxID=2100; P115 MYCHR STANDARD; PRT; 979 AA. P41508; 01-NOV-1995 (Rel. 32, Created) 01-FBB-1996 (Rel. 33, Last sequence update) 28-FBB-2003 (Rel. 41, Last annotation update) P115 protein. RESULT 10
P115 MYCHR
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740 LTLEAASEQYSLDLDIEQARHFVDSLKKELKELGNVNLEAITEFEEVNQR----YQEKKQ 795
                                                    597 HYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKD----IRKILSGYIVEIEDTEG
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      entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 ---PKTEVE------SSIQEITSKLDNLKNALSEINLQBARIEBRRKLIISGEIV-V 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       443 LGAALNQIVMKTSEDVLQAIDFLKKNLSGKATFIPLTSIKEREVREDHLLVLKGQKGFLG 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              387 KNQTLATIKAKENQ----LSQILAPNNYYPSKNLAPI--------ALN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 BOSAKOLRGINMDDVIFAGSKTVKPQEKAMVKLTFKNEDAIBETKOIFTISRLLKRGQGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 NOYFOS-----AIMSGFIKVKKSDEYTFATSADNHVTMWVDDQE--VINKASN 102
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                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.3%; Score 162.5; DB 1; Length 979;
Best Local Similarity 18.9%; Pred. No. 0.81;
Matches 175; Conservative 133; Mismatches 341; Indels 277; Gaps
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169 224 COILED COIL (POTENTIAL).
231 400 COILED COIL (POTENTIAL).
659 821 COILED COIL (POTENTIAL).
884 912 ALA/ASP-RICH (DA BOX).
979 AA, 110566 MM, 30D51C56B56280F4 CRC64;
                                                                      PIR, JQ0894, JQ0894.
InterPro; IPR003499; ABC transporter.
InterPro; IPR003499; ABC transporter.
InterPro; IPR003495; SWC C.
InterPro; IPR003395; SWC C.
InterPro; IPR003395; SWC N.
IPfam; PR02463; SWC C.
IPfam; PR02463; SWC N; I.
ITGRRAMS; TIGR00650; MG442; 2.
ATP-binding; Coiled coil.
                                                          EMBL; M34956; AAA25423.1; -.
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SEQUENCE
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01-APR-1993 (Rel. 25, Last sequence updat
10-OCT-2003 (Rel. 42, Last annotation upd
Reticulocyte binding protein 1 precursor.
                                                                                                        ---GLNTADTA-RLNANIRYVNTG-
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  detected action on small molecule substrates.

OCRACTOR: Binds 1 zinc ion per subunit (By similarity).

SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H). The light chain has the pharmacological activity, while the N- and C-terminal of the heavy chain mediate channel formation and toxin binding, respectively.

SUBCELLULAR LOCATION: Secreted.

MISCELLANDEOUS: There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, Cl, D, E, F, and G.

MISCELLANDEOUS: BOTULINUM TYPE D NEUROTOXIN IS SYNTHESIZED BY D STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE

BACTERIOPHAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQYNVKRRTHYFSRHYLPVFANILDDNIYTIRDGF---NLTNKGFNIE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Hydrolase, Metalloprocease, Zinc.
Hydrolase, Metalloprocease, Zinc.
BOTULINUM NEUROTOXIN D, LIGHT-CHAIN.
BOTULINUM NEUROTOXIN D, HEAVY-CHAIN.
ZINC (CAPALYIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYIC) (BY SIMILARITY).
INTERCHAIN (PROBABLE).
ND -> PV (IN STRAIN D-SA).
K -> Q (IN STRAIN D-SA).
K -> T (IN STRAIN D-1873).
K -> T (IN STRAIN D-1873).
K -> D (IN STRAIN D-1873).
K -> N (IN STRAIN D-1873).
K -> N (IN STRAIN D-1873).
K -> N (IN STRAIN CB16).
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                                                                                                                                                              SIMILARITY: Belongs to peptidase family M27.
                                                                                                                                                                                                                                                                                      Conservative 117;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-eib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            477 WSEVLPQIQETTARIIFNGKD--LNL------VERRIAAVNPSDPLETTKPDMTL 523
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                                                                                                                                    NYNQFLELEK------TKQLRLDTDQVYGNI-----ATYNFENGRVRVDTGSN
                                                                                                                                                                                                                                                                                                                                                     ILSGYIV---EIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLY---ISNP
----LPNVNMBPLNLPGEBIVFYDDITKYVDYLNSYYYLESQKLSNNVENITLTSVEEA
                                                              -----TAPIYNVLPTTSLVLGKNOTLATIK
                                                                                                                                                                                  ------AKENOLSQILAPNNY----YPSKNLAPIALNAQKDFSSTPITM
                                                                                                                                                                                                                      688 NCLEQRVKRWKDSYQWMVSNWLSRITTQFNHINYQMYDS-----LSYQADAIKAKIDL
                                                                                                                                                                                                                                                                                            741 EYKKYSGSDKENIKSQVENLKNSLDVKISEAMNNINKFIRECSVTYLFKN-----
                                                                                                                                                                                                                                                                                                                                                                                                     524 KEALKIAFG-FNEPNGNLQYQCKDITEFDFNFDQQTS----QNIKNQLAELNATNI-YTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRK
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                                         HGNAEVHASFF-----DIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETM-----
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=31273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Barnwell J.W.;
Plasmodium vivax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-22315339; PubMed=1617731;
MAINSKI M.R., Medina C.C., Ingravallo P., I
"A reticulocyte-binding protein complex of I
merozoites."
CE11 69:1213-1226 (1992).
- I- FUNCTION: Involved in reticulocyte adhe
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Tue May

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2060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2419 IDRIN--ALMDDIBIFKKEN-----NYNLMEVNIETIHRVNDYIEKIINKLVQAKTE
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                                                                                                                                                                                                                              123 ENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDG
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                                                                                                                                                                  1944 NSMYESMVTLANYFLSDEAKISSGMEFNAEMKSNFKTDLELEIFSV----ISNSNEL---
                                                                                                                                               10 NESESSSOGLLGYYFSD-----LNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQS
                                                                                                                                                                                                                                                 E-----FNEXLEEAKNKEEVVS------BKVREALKRLS------
                                                                                                                                                                                                                                                                      183 IPDSLEVEGYTVDVKNKRTFLSPWISNIHE----KKGLTKYKSSPEKWSTASDPYSDFEK
                                                                                                                              Gaps
                                                                                                                             209;
              POTENTIAL.

RETICULOCYTE BINDING PROTEIN 1.

EXTRACELLULAR.

POTENTIAL.

CYTOPLASMIC.

CELL ATTACHMENT SITE (POTENTIAL)

CELL ATTACHMENT SITE (POTENTIAL)

CELL ATTACHMENT SITE (POTENTIAL)

13 MW; B9DBE442205EBCF CRC64;
                                                                  (POTENTIAL).
(POTENTIAL).
CRC64;
                                                                                                         2869;
                                                                                                         Length
                                                                                                                             Indels
                                                                                                         4.2%; Score 159.5; DB 1;
larity 18.4%; Pred. No. 4.8;
Conservative 142; Mismatches 297;
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LNSVLEAAI-QKRG 2600
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         Malaria; Receptor; Signal;
EMBL; M88097; AAA29743.1;
                                     18 280
2808 282
2827 286
1030 103
2599 260
2869 AA;
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                                                                                                         Query Match
Best Local Simi
Matches 146; (
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674 689 TYSKSNYMIRDCFQNN -> DLFKIKLYDTRIVSKIM (IN REF. 2 AND 3).
814 815 DY -> EL (IN REF. 2 AND 3).
818 822 RYSSN -> PDIQVI (IN REF. 2 AND 3).
1000 AA, 114980 MW, AD4FBF0BC7C588D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96220458; PubMed=8649382;
Luke M.M., della Seta F., di Como C.J., Sugimoto H., Kobayashi R.,
Arndt K.T.;
"The SAP, a new family of proteins, associate and function positively
with the SIT4 phosphatase.";
Mol. Cell. Biol. 16:2744-2755(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96287652; PubMed=8686379; Bki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Bki T., Naitou M., Hagiwara H., Ozawa M., Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Shibata T., Hanoka F., Murakami Y.; Sasanuma M., Tsuchiya Y., Shibata T., Hanoka F., Murakami Y.; Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI from Saccharomyces cerevisiae."; Yeast 12:149-167(1996).

-:-FUNCTION: Associates with the SIT4 phosphatase in a cell cycle dependent manner. May be directly or indirectly involved in SIT4-dependent functions in budding and in normal G1 cyclin
                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Bukarychis Fugaty, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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4.2%; Score 159; DB 1; Length 1000;
Best Local Similarity 19.4%; Pred. No. 1.2;
Matches 172; Conservative 128; Mismatches 324; Indels 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=S288c / AB972;
MEDLINE=95400292; PubMed=7670463;
MUTAKAMI Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma S.-1.; Sasanuma M., Teuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.;
"Amazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- PTM: Hyperphosphorylated in the absence of SIT4.
                                                       01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
28-FBE-2003 (Rel. 41, Last annotation update)
SIT4-associating protein SAPIS5.
SAPIS5 OR YFR040W.
1000 AA
PRT;
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EMBL; D50617; BAA09279.1; --
Germonline; 140194; --
SGD; S0001936; SAP155;
InterPro; IPR007587; SAPS.
Pfam; PP04499; SAPS; 1.
Phosphorylation; Cell cycle.
CONFLICT
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SEQUENCE OF 98-1000 FROM N.A.
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STANDARD;
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1 EVKQENRLINESESSSQGLLGYYFS--DL----NFQAPMVVTSSTTGD-----LSIPS

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FROM N.A.

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717 MDFSYNSFLVLSLFNLKSSYQFMTDIVISDEKGTDVSRFSPVIRDPNFDFKITTDFILRG 776
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                                                                                                                 204 DLNN-----LIDYQEQQQLD------DSSQEDVYVESDTEQEEKEDDNNSNNKK
                                                                                                                                               R----STSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSP-----WISNIHEKKG
                                                                                                                                                              LTKYKSSPEK-WSTASDPYSDFEKVTGRIDKOVSPEARHPLVAAYPIVHVDMENIILSKN
                                                                                                                                                                                                                                                                                                            STSRIHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAI-DHSLS--LAGERTWAETM
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                                                                                            RLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKK
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1D FATL SCHPO

AC 013735; 09UT00;

DT 15-UL-1998 (Rel. 36, Created)

DT 28-FBE-2003 (Rel. 40, Last sequence update)

DT 38-FBE-2003 (Rel. 41, Last annotation update)

DT Actin interacting protein 3 homolog.

GN FATI OR SPACISAIO.16 OR SPACISEI.01.

S Schizosaccharomyces pombe (Fission yeast).

C Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

CC Schizosaccharomyceales; Schizosaccharomycetaces.

CC Schizosaccharomyces. RESULT 14

33;

202;

Score 159; DB 1; Length 1385; Pred. No. 1.9; 5; Mismatches 293; Indels 205

Query Match Best Local Similarity, 19.2%; Pre Matches 147; Conservative 125;

.92 326 75 384

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DLNFQAPMVTSSTTGDL----SIPSSELENIPSENQYFQSAIWS----GFIKVKKS

DEYTFATSADNHVTMWVDDQEVINKAS---

-- NSN 104

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MEDILINE=20143585; PubMed=10679021;

MEDILINE=20143585; PubMed=10679021;

MEDILINE=20143585; PubMed=10679021;

"The secretory pathway mediates localization of the cell polarity regulator Aip3p/Bud6p.";

Mol. Biol. Cell 11:647-661(2000).

-!- FUNCTION: Involved in the organization and/or function of the actin cytoskeleton.

-!- SIMILARITY: TO YEAST BUD6. EMBL, 297208; CAB10112.1; -.

EMBL, AL109770; CAB52420.1; -.

GeneDB SPombe; SPAC13A10.16; -.

GO; GO:0005884; C:actin filament; ISS.

GO; GO:0016643; P:cell organization and biogenesis; ISS.

InterPro; IPR005613; AIP3.

Pfam; PF03915; AIP3; 1.

Poined coil; Cytoskeleton.

COILED COIL (POTENTIAL).

SEQUENCE 1385 AA; 154325 MW; ABB3D40CC4FF7537 CRC64; 

oy Ob	105 KIRLEKGRLYQIKIQYQRBN- 	KIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKK 	143 499	
ò	144 EVISSDNLQLPE	SSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSL	187	
Op	500 ELLERQIQKAESSEDTSEIES	ELLERQIQKAESSEDTSEIESLQGKLSLPQVSSTQQEIQPSSSVPEAASNEIAEKEPAVT	559	
ò	188 EVEGYIVDVKNKRIFLSPWIS	EVEGYTUDVKNKRIFLSPWISNIHEKKGLIKYKSSPEKWSTASDPYSDFEKVTGRIDKNV	247	
Op	560 AIESITERKEEAPVIS	AIESITERKEEAPVISSSEKIESGTSISTSDTKGGLANFENDSLEELERLIQQN-	613	
δλ	248 SPEARHPLVAAYPIVHVDMEN	SPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNA	307	
Db	614 NAEQDEPSYKFHKYEYSSEE-	:     :     :     :       :	699	
ò	308 EVHASFFDIGGSVSAGFSNSN	EVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETWGLNTADTARLNAN	363	
ДÞ	670 NTGASAKLINDP	SAKLINDPSSTITVSDVYPKKPASPVBITEPPSSALVSATSPTTNVP	720	
δ	364 IRYVNTGTAPIYNVLPTTS	I RYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIAL	421	
ΩD	721 IVPEAVHLSTAFSTAPVSTIV-	ddNISPLPTVAP	753	
δ	422 NAQKDFSSTPLTMNYNQFL	NAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNW	477	
QQ	754 NVSGSPSETPISKPEKVPVVS		811	
à	478 SEVLPQIQETTARIIFNGK	SEVLPQIQETTARIJENGKDLNLVERRIAAVNPSDPLETTKPDMT-LKEALKIAFGFN	534	
Dp	812 ANELGELFSNVYKISFSGDSYELNIED	PDTKISYLLEDLSDLKYKSLVSFMFK	864	
ò	535 EPNGNLOYQGKDITEFDF	EPNGNLOYQGKDITEFDFNFDQQISQNIKNQLAELNATNIYT-VLDKIKLNAKMNIL	290	
qq	865 EQDANKKREDFHSGEVSAIQH		917	
ò	591 IRDKRFHYDRNNIAVGADESV	IRDKR FHYDRINI AVGADESVVKEAHREVINSSTEGLLLINI DKDIRKI LSGYIV-EIEDT	649	
qq	918IEQNIST	: :     :     :     :	954	
ò	650 EGLKEVINDRYDMLNISSLRODGKTFI	GKTFIDFKKYNDK 684	,	
g	:  :   :  :   955 KFYQQVKNMQLELASLKQ	: ::    ::   ::    ::  KFYQQVKNMQLELASLKQISAAFPTRIPLKIKDFKKEINAFNEK 998		
RESULT CAGA H	LLT 15 A HELPJ			
O A	CAGA HELPJ STANDARD; O9ZLT1:	PRT; 1167 AA.		
ם	(Rel. 40, Creat (Rel. 40, Last	ed) sequence update)	-	
DT DE	16-OCT-2001 (Rel. 40, Last annotation of Cytotoxicity associated immunodominant	annotation update) unodominant antigen (120 kDa protein)		
E C	(CAG nathogenicity island protein 26)			

tills D.M., Ives C., Taylor D.E., Vovis G.F., (CAG pathogenicity island protein 26).
CAGA OR CAI OR CAG26 OR JHP0495.
Halicobacter pylori J99 (Campylobacter pylori J99).
Bacteria, Proteobacteria, Epsilonproteobacteria; Campylobacterales; two unrelated isolates of the human P. C. SEQUENCE FROM N.A.
SECURICE FROM N.A.
MEDLINE=99120557; PubMed=9923682;
Alm R.A., Ling L.-S., Moir D.T., King B.L., Brown B.D., Doig F Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G., Tummino P.J., Carueo A., Uria-Nickelsen M., Mills D.M., Ives C. Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis Trust T.J.;

Trust T.J.; Trust T.J.;
"Genomic sequence comparison of two unrelated isolates of "Genomic sequence comparison of two unrelated isolates of gastrio pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-!- FUNCTION: MAY BE NECESSARY FOR THE TRANSCRIPTION, FOLDING, OR FUNCTION OF THE CYTOTOXIN. NCBI_TaxID=85963; 

EXPORT,

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4.2%; Score 158.5; DB 1;
Best Local Similarity 19.7%; Pred. No. 1.6;
Matches 158; Conservative 149; Mismatches 308; LRODGKTFIDF----KKYND--KLPLYISNP PIR; B71924; B71924. InterPro; IPR005169; CagA. InterPro; IPR004355; IVSec_cagA. Pfam; PR03507; CagA; 1. PRINTS; PR01553; TYPE4SSCAGA. EMBL; AE001483; AAD06073.1; -. Antigen; Complete proteome. DOMAIN 246 249 1167 AA; 22 591 156 636 742 323 382 843 442 891 502 SEQUENCE 66 DOMAIN 음 9 6 7 8 8 8 8 8 셤 ठ 셤 8 a 8 a ઠે ò g ò g ò 유 ò

1092 APLSAYDKIGFNQKNMKDYSDSFKFSTRLSNAVKDIKSGFVQFLTNIFSMGSYSLMKASV 1151

712 ENGDISTNGIKKILIFSKKGYE 733 |:| :| | :| | :: 1152 EHGVKNIN-----TKGGFQ 1165

 Search completed: May 3, 2004, 19:36:51 Job time : 13.2539 secs

# GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

May 3, 2004, 19:30:17 ; Search time 34.6261 Seconds (without alignments) 6697.424 Million cell updates/sec	US-09-848-909A-8 3773 1 EVKÇENRLLNESESSSQGLLTSTNGIKKILIFSKKGYEIG 735		
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004, 19:30:17	-909A-8 LLNESESSSQGLL	BLOSUM62 Gapop 10.0 , Gapext 0.5	1017041 seqs, 315518202 residues
May 3, 20	US-09-848-909A-8 3773 1 EVKQENRLLNESES		1017041 8
Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

1017041

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	Description	Q937w2 bacillus an	Q937w3 bacillus an		006498 clostridium	29kh41 clostridium			Q844j8 bacillus th	28kyk2 bacillus an	Q8rgk2 fusobacte:	18ii04 plasmodium	Q9pq08 ureaplasma	18iks2 plasmodium	28ihy4 plasmodium	28rjn9 mycoplasma	Q897h6 clostridi
277	L		ū	U	O	•		0	•	0		•		0		0	
	Ð	Q937W2	0937W3	032739	006498	Q9KH41	046221	086171	Q844J8	Q8KYK2	Q8RGK2	OBII04	092008	Q81KS2	Q8IHY4	Q8RJN9	0897н6
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	* Query Match	97.9	97.9	23.4	23.4	23.4	23.5	21.7	19.5	7.9	5.8	5. 9.	5.4	5.4	5.3	5.1	5.1
	Score	3695	3695	883.5	883.5	881.5	877	819	734	296.5	220.5	217.5	205	202.5	199.5	194	191.5
	Result No.	; ; ; ;	7	ო	4	S	9	7	80	σ	10	11	12	13	14	15	16

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Q8WSK5	Q8IHP9	Q8ICP9	026216	QBISA6	Q814R2	OBNWQ6	Q81548	Q9BJX9	Q8IHQ2	Q8IB09	Q26223	025579	Q8IC27	Q8IL45	O98PM9	Q7YWE7	Q7YWE6	Q9 ZHL3	Q7VLE8	081GX1	Q99U54	Q931R6	Q7WZI3	Q8IHV4	Q9U4X0	Q813Z1	Q9RM77	081500
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5.1	5.1		5.0							4.9		4.0	6.9	4.9	4.9	4.9	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	٠	4.8	4.8	4.8
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# ALIGNMENTS

RESULT 1

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	M., ulenco	<u>.</u>	; °
, te)	Bacillus anthracis.  Plasmid pxol.  Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.  NCBL_TAXID=1392;  [1]  SEQUENCE FROM N.A.  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAIN=Ferrara;  STRAI	databases.	
; 741 AA. ed) sequence update) annotation update)	ceae; B	accline Birain ca L/GenBank/DDBJ da mal DNA; IEA. y; IEA. YiEA. xinB. C7F95820B73065C0	Pred. No. 7.4e-168; ; Mismatches 2;
741 AA. ) quence up notation	Bacillaceae; Marianelli C F.; coding for th	1116 SLIC enBank/I DNA; II EA. B.	Pred. No. 7.4 Mismatches
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23.4%; Score 883.5; DB 2; Length
Best Local Similarity 28.8%; Pred. No. 4.4e-34;
Matches 260; Conservative 147; Mismatches 258; Indels
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Tribosyltransferate) Dia complete binary toxin (actin-specific ADP-ribosyltransferate) Dy Clostridium difficile CD196.";

Infect. Immun. 65:1402-1407(1997).

R MEBL, 176081; AAB67305.1; -.

R HSSP; P13423; 1ACC.

R GO; GO:0005576; C:extracellular; IEA.

R GO; GO:0015707; P:toxin activity; IEA.

R GO; GO:0016707; P:toxin activity; IEA.

R GO; GO:0016707; P:toxin activity; IEA.

R GO; GO:0016707; P:toxin activity; IEA.

R GO; GO:0016705; P:pathogenesis; IEA.

R Pfam; PF03495; Binary toxis.

R Pfam; PF03495; Binary toxis.

R Pfam; PF03495; Binary toxis.
                                                                                                                                                                                                                         Clostridium difficile.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
Clostridium.
NCBI_TaxID=1496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.4%; Score 883.5; DB 2; Length 876; Best Local Similarity 31.7%; Pred. No. 4.4e-34; Matches 252; Conservative 139; Mismatches 279; Indels 125;
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                                     Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CD196;
MEDLINE-97230316; Pubmed=9119480;
                                     (TrEMBLrel. 0 (TrEMBLrel. 0 (TrEMBLrel. 2)
                                                                                                                                                                          ADP-ribosyltransferase.
                                     01-JAN-1998 (
01-JAN-1998 (
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320 337

Closrridium difficile. Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium. NCBI_TaxID=1496; Last sequence update) Last annotation update) Ą 876 Created) (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 24, PRELIMINARY; 01-OCT-2000 ( 01-OCT-2000 ( 01-JUN-2003 ( RESULT Q9KH41 SOOR BEAUTION OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF T

[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=CCUG 20309; Chang S.Y., Song K.P.; "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain CCUG 20309;"; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF271719, AAF81761.1; -. HSSP, P13423; 1ACC.

GO; GO:0005576; C:extracellular; IEA.
GO; GO:0015070; R:toxin activity; IEA.
GO; GO:001509465; P:pathogenesis; IEA.
InterPro; IPR003896; Anthrax.toxinB.
Pfam; PF0495; Binary toxBi.
PRINTS; PR01391; BINARYTOXINB.
SEQUENCE 876 AA; 96793 MM; 366D62F352E745A5 CRC64;

30; 222 206 FDFKLMSDWEDEDLDTDNDNIPDSYERNGYTI----KDLIAVKWEDSFAE-QGYKKYVSN 260 514 539 : | |::|: ||::|| |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || | NIYTVLDKIKLNAKMNILIRDKRFHY---DRNNIAVGADESVVKEAHREVINSSTEGL-- 627 652 706 AIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQR 122 EN--PTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKOKSSNSRKKRSTSAGPTVP---- 176 PEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTONT 282 337 422 454 62 66 599 KIYNV----KLERGMAILIKTPTYPTNFDDYNNYP--STWSNVNTTNKDGLQGSANKLNG VYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPL ETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITE--FDFNFDQQTSQNIKNQLAELNAT -----LINIDKDIRKILSGY-----IVEI----EDTEGL-----KEVI ETKIKIPMSELKPYKRYVFSGYSKDPLTSNSIIVKIKAKBEKTDYLVPEQGYTKFSYEFE NDRYDMINIS-SLRQDGKTFIDFKKYND--KLPLYISNPNYK-----VNVYAVTKENT TTEKDSSNIEITLIGSGTTYLDNLSITELNSTPEILDEPEVKIPTDQEIIDAHKIYFADL --- DRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS KAKENOLSOILAPINNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQ KKKEIVNEDILPNNGLMGYYFTDEHFKDLKLMAPIKDGNLKFEEKKVDKLLDKDKSDVKS DSETRIISKWISTSRIHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHS----4 QENRILINESESSSOCILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN-IPSENQYFQS ---LSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNOTLATI Gaps 125; Length 876; Indels ch 23.4%; Score 881.5; DB 2; Il Similarity 31.6%; Pred. No. 5.5e-34; 251; Conservative 140; Mismatches 279; IINPSENGDŢSTŅGI 721 NFNPS-TGNTYINGM 786 Query Match Best Local S: Matches 251 123 261 364 395 423 455 483 515 540 573 653 657 707 177 223 283 318 338 628 à g g 요 g ò g qq ઠે Сþ Ś g 8 g ò ò ò 셤 8 셤  $\dot{\delta}$ g à à g ð

01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last sequence update)
01-UDN-2003 (TrEMBLrel. 24, Last annotation update)
10ta toxin component 1b precursor.
Clostridium perfringens.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
NCBI_TAXID=1502; PRT; PRELIMINARY; 046221 RESULT 6
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119 -QYQRENPTEKGLD-FKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTV- 175
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KE SEQUENCE FROM N.A.

C STRAIN=type C;

KEDINIE=$6184657; PubMed=8645309;

KEDINIE=$6184657; PubMed=8645309;

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KEDINIE=$6184657; PubMed=8645309;

KEDINIE=$6184657; Parament-I gene of botulinum C2 toxin and PCR detection of its gene in clostridial species.";

KEDINIE=$6184657; Parament-I gene of botulinum C2 toxin and PCR detection of its gene in clostridial species.";

KEDINIE=$6184657; Parament-I gene of botulinum C2 toxin and PCR detection of its gene in clostridial species.";

KEDINIE=$6184657; Parament-I gene of botulinum C2 toxin and PCR HSSP; P13423; LACC (SEXTRACHILL) IEA.

CO: GO: 0015070; Proxin activity; IEA.

CO: GO: 0015070; Proxin activity; IEA.

CO: GO: 0015070; Proxin activity; IEA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KOENRLINESES -- SSOGLIGYYFSDINFOAPMVVTSSTTGDLSIPSSELENIPSENQYF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 EQLMSENQLLKNYEGIKLYWETSDIIKEIIPSEVL----LKPNYSNTNEKSKFIPNNTLF
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586 IIKEQLKYLDDKKIYNV----KLERGMNILIKVPSYFTNFDEYNNFP--ASWSNIDTKNQ
                                                                                                                                                                     700 EKÖYTKFSYEFETTGKDSSDIEITLTSSGVIFLÖNLSITELNSTPEILKEPEIKVPSDQE
                                          618 EVINSSTEGL-----LLNIDKDIRKILSGY-----IVEIEDTEGLKEVIND
                                                                    ---SLRODGKTFIDFKKYND--KLPLYISNPNYKV----
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Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
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MEDLINE=98323874; PubMed=9659689;
Kimura K., Kalota T., Obishi I., Isogai H., Isogai E.,
Kimura K., Kucomponent-II of botulinum C2 toxin.";
Vet. Microbiol. 62:27-34(1998).
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Last sequence update)
Last annotation update)
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                                                                                                                                      659 RYDMLNIS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 IQDKOLGSIDNLSVP-----KLYW-ELNGNKTVIPEENLFFRDYSKIDEND----- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGPTVP------DRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIH 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 SKNEDOSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSST 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQ 119
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                                                                                                                        toxin genes and
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                                                                                                                                                                                                                                                          Popoff M.R.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 POTENTIAL.
875 IOTA TOXIN COMPONENT IB.
98468 MW; C9AE092CD3818921 CRC64;
                         SEQUENCE FROW N.A.
STRAIN-NCIB 10748;
MEDLINE=94041637; PubMed=8225592;
Perelle S., Gibert M., Boquet P., Popoff M.R.;
"Characterization of Clostridium perfringens icta i expression in Escherichia coli.";
Infect. Immun. 61:5147-5156(1993).
                                                                                                                                                                                                                                                                                               EMEL, X33562; CAA51960.1; EMEL, X33562; CAA51960.1; EMER, 140862; 140862. HSSP, P13423; 1ACC. GO, GO:0005576; C:extracellular; IEA. GO; GO:0015070; F:toxin activity; IEA. GO; GO:0019076; P:pathogenesis; IEA. InterPro; IPR003896; Anthrax_toxinB. Pfam; PF03495; Binary tox8; T. PRINTS; PR01391; BINARYTOXINB.
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212 8
875 AA;
                                                                                                                                                                                                                                    STRAIN-NCIB 10748;
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283 DSETRIISKNISTSRTHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
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Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Read T.D., Salzberg S.L., Pop M., Shumway M., Umayam L., Jiang L.,
Holtzapple E., Busch J.D., Smith K.L., Schupp J.M., Solomon D.,
Keim P., Fraser C.M., Sequencing for Discovery of Novel Polymorphisms in
Bacillus anthracis.";
Science 296:2028-2033(2002).
SmBL, AE011190; AAM26108.1;
GO; GO:0046821; C:extrachromosomal DNA; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 PYQAHTVGDPYTDWEKAAGDIPKSNAAATRNPLVAAFPSINVDMRKMILSKDSNLS----
                                                                                                                                                                                                                                                                                                  324 -----NSAEAHSNNSYTYANSE------GASIEAGFGPKGFSFGVSANYQHTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       516 TTKPDMTLKEALKIAFG---FNEPNGNLQYQGKD----ITEFDFN-----FDQQTSQN
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    QXMKRDIDED----TDTDGDSIPDLWEENGYT--IQNK--VAVKW-DDKFAQQGYVKYLSS
                                                                               223 PEKWSTASDPYSDPEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
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NCBI_TaxID=1392;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Protective antigen-related protein, (pX01-111).
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                                                SIJGDYLNPGGTYPIJGEPPMALNTMDQFSSRLIPINYNQLKSIDNGGTVMLSTSQFTGN 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          460 FAXYN-SNGNLVTD-GNNWGPYLGTIKSTTASLTLSFSGQTTQVA---VVAPNFSDPEDK 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 TKPDMTLKEALKLAFGFNEPNGNLQYQGKDIT---EFDFNFDQQTSQNIKNQLAELNATN 573
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                                                                                                                                                              TRIISKNISISRIHISEVHGNAEVHASFFDIGG-----SVSAGFSNSNSSTVAIDHSL 338
                                                                                                                                                                                                                                    287 TKSMSKSTSHSSTNINTV--GAEVSGSLQLAGGIFPVFSMSASANYSHTWQNTSTVDDT- 343
                                                                                                                                                                                                                                                                                                                        339 SLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKE 398
                                                                                                                                                                                                                                                                                                                                                                                                       344 --TGE-SFSQGLSINTGESAYINPNIRYYNTGTAPVYNVTPTTTIVIDK-QSVATIKGQE 399
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"Cloning of vipla(C) and vip2A(C) from Bacillus thuringiensis HD201.";

Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.

BMBL, AY245547, AA086514.1;

GO; GO:0005576; C:extracellular; IEA.

GO; GO:0015070; F:toxin activity; IEA.

GO; GO:000465; P:pathogenesis; IEA.

InterPro; IPR03896; Anthrax toxinB.

PRIM: PR03495; Blnaty toxB; I.

PRIMTS; PR01391; BINARYCOXIN.

SEQUENCE 775 AA; 87110 MM; 416B2S394361B731 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus thuringlensis.
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
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01-JUN-2003 (TREMBLEEL 24, L.
01-OCT-2003 (TREMBLEEL 25, L.
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671 DGKTF-----IDFKK--YNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIK 722 790 DIKANNGILQAIK-----NINIKISNDLKLDGKYTANDSLNINAKSLENNGN--- 836 544 SNNLSSNNINNSKNIFVNGNLKISNNLNNSGVIEGLELNTNSIENTGNITIKNKLTSQNL 603 294 STSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVA---IDHSLSLAGERTWAETM 350 351 GLNTAD-----TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQ 403 625 EGLLL------NI-DKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQ 404 ILAPNNYYPSKNIAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYN 464 FENGRVRVDTGSNWSEV-----LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 604 NNKK-----NTANVNAGFLDVHNKISS-VGNIKAITMKINNLDNSGNIL-----TN 1000 DÍ 1001 688 516 576 240 183 RESULT 11 g à g ઠે 6 B q ሯ qq à ብ ራ g ⋩ q 챵 В ∂ 37; 112 246 QAPMYATKGDVVISSKGKVYLKDTQAKRDIKİSSTETEIGSKLLAENALNIKSGKTSNSG 305 OIRANNNITINGNVDSSNLIFTNKDITISGNLKNSGNVSSSNLNVKEIENSNKVVVEE-K 364 161 LSSTKITNLGNLSAKEIEKTNIFNSGKLFSKNITAKDFKNNGEV-SSENLTTTNLENSNK 423 424 INVKENINSNSIVNKTNAEITSKMLNTNNLDNRGNITIINNVSSGVIANNGKLLVGNTIN 483 69 672 113 KTFIDFKKYNDKLPLYISNPNYKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKG 731 LYQIKI------QYQRENPTEKGLDFKLYWT--DSQNKKEVISSDNLQLPELKQKSS 70 KVKKSDEYTFATSADNHVTMWVDDQEVIN--------KASNSNKIRLEKGR 30 QAPMVVTS----STTG-----DLSIPSSELE---NIPSENQY-FQSAIWSGFI ESUJENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ATCC 2586;

MEDLINE-21865394; PubMed=11889109;

MEDLINE-21865394; PubMed=11889109;

MEDLINE-21865394; PubMed=11889109;

MAGARTAI V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Battacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., A Jarsen V., Chu L., Kogan Y., Giaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walluras T., Pusch G., Haselkorn R., Ronstein M., Kyrpides N., Overbeek R.;

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M. GO; GO:0006023; F:peptidase activity; IEA.

GO; GO:000623; F:peptidase activity; IEA.

GO; GO:0006208; Hemmbrane; IEA.

GO; GO:0006209; Peptidase activity; IEA.

InterPro; IFR001659; Peptidase 226.

InterPro; IFR001659; Peptidase 226.

InterPro; IFR001659; Peptidase 226. Query Match
5.8%; Score 220.5; DB 16; Length 1881;
Best Local Similarity 20.8%; Pred. No. 0.04;
Matches 175; Conservative 131; Mismatches 303; Indels 233; Gaps 1 MESLGINNIYNALDRIKLNAKMNILVRDP-YHYDNNGNIVGVDDSYLKNAYKQILNWSSD -----NSRKKRSTSAGPTVPDRDNDG------Hemolysin. FN0291. Fusobacterium nucleatum (subsp. nucleatum). Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae; 1881 AA; 204375 MW; D635156A4EFA4877 CRC64; Last sequence update) Last annotation update) GLLLNIDKDIRKILSGYIVEJEDTE-----Created) Pfam; PF05860; Haemagg_act; 1.
Pfam; PF0018; SH3; 1.
PROSTIE; PS00761; SPASE_I_3; 1.
Complete proteome.
SEQUENCE 1881 AA; 204375 MW; 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25, PRELIMINARY; Fusobacterium. NCBI_TaxID=76856; YEI 734 XEI 174 306 365 Query Mac. 113 162 626 9 673 732 172 Q8RGK2 RESULT 10
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---IPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKV

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TGRIDKNVSPEARHPLVAAYPIVHVDMEN-----IILSKNEDQSTQNTDSETRTISKNT

670

08.104; 01-MAR-2003 (TrEMBLrel. 23, Created) 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical protein. Plasmodium falciparum (isolate 3D7). Blasmodium Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TAXID=36329; PRT; 3468 AA. PRELIMINARY;

Ureaplasma parvum (Ureaplasma urealyticum biotype 1). Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma. NCBI_TaxID=134821;

Ε.Υ.,

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N [1]
SEQUENCE FROM N.A.
STRAIN=SECOVAT 3; PubMed=11048724;
MEDLINE=20500219; PubMed=11048724;
A Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.M. Cassell G.H.;
A Cassell G.H.;
I "The content sequence of the mucosal pathogen Ureaplasma urealyticum.";
I Nature 407:757-762(2000).
I EMBL; AE00245; AAF30894.1; -.
M Hypotherical protein; Complete proteome.
SEQUENCE 4688 AA; 534880 MW; B53ABFAFFEE1997E CRC64;
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5.4%; Score 205; DB 16;
Best Local Similarity 21.3%; Pred. No. 0.71;
Matches 174; Conservative 132; Mismatches 324;
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                                          Ouery Match
5.8%; Score 217.5; DB 5,
Best Local Similarity 19.0%; Pred. No. 0.12;
Matches 159; Conservative 131; Mismatches 274;
EMBL, AE014841, AAN35955.1, -. Hypothetical protein. SEQUENCE 3468 AA; 411913 MW;
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PATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTD

19 LLGYYFSDLNPQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYT

4415 4017 4197 3851 3907 DVTSDFKEGTWAHDLSNSVNFKEETTYKLVKIQFVNKPTKAKNNINNSENNVILDNTNSI 4077 :|:: | |:: | |::| | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: | STSRIHTS-EVHGNAEVHASF----FDIGGSVSAGFS----NSNS---SIVAID INLVERRIAAVNPSDPLETT-----KPDMTLKEA-----LKIAFGFNEPNGNLQ -----RINIAVGA---DESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTE YQLLSNLNSN------REYRFEKIEINHISNTNNFEDLEKLNGVSNTFITQTKNT -----TIKAKENQLSQILAPNNYYPSKNLAPIALN-AQKDFSSTPITMNY--NQFLELE | :: ::::: | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : SONKKEVISSDNLOLPELKOKSSN----SRKKRSTSAGPTVPDRD-------IQTQNDTINDTQQTINVTLSGVNSK-YNGRQİKVVYXDNNNVİYESS---LITLQKGKND FEXVIGRIDANVSPEARHPLVAAYPIVHVDMENIILSKN-EDQSTQNTDSET-RIISKNT HSLSLAGERIWAETMGLNT---ADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLA NSNYEFITKVGDHKLINITSSNNVNTNSQTINFTLSGVKKSWVGKKIKLSYKSNDTSESI KTKOLRLDTDQVYGNIATYNPENGR-----VRVDTGSNWSEVLPQIQETTARIIFNGKD YQGKDITEFDFNFDQQTSQNIK-NQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYD-----NDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSD GLKEVIND--RYDMLNISSL-RQDGKTFIDF-----KKY---1078 1305 1258 4198 542 3852 3908 3958 139 180 236 294 336 4018 393 444 498 900 g 8 8 8 8 6 8 6 8 6 셤 ò d ઠ 임 ò 음 장 g & ઠે

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0.1-OCT-2000 (TrEMBLrel. 15, C)
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0.1-OCT-2003 (TrEMBLrel. 23, Li
Hypothetical protein UU482.

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 24, Last annotation update)
Ferlin, putative.
PF14 0530.
PB14 0530.
Blasmodium falciparum (isolate 3D7).
Eukaryots, Alveolata, Apicomplexa; Haemosporida; Plasmodium. Query Match 5.4%; Score 202.5; DB 5; Length Best Local Similarity 19.8%; Pred. No. 0.29; Matches 174; Conservative 128; Mismatches 328; Indels Nature 419:498-511(2002).
BMBL, AB014825, AAN37143.1; -.
InterPro; IPR000008; C2.
Pfam; PF00168; C2; 5.
SMART; SM02239; C2; 5.
PROSITE; PS50004; C2 DOMAIN 2; 2.
BRQUENCE 1904 AA; -224720 WWW; AA36470367BDEC41 CRC64; 4416 SNKLP-KLNNINYQIK---INKSHTII--SKNGEWS NDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS PRT; 1904 AA PRELIMINARY; SEQUENCE FROM N.A. falciparum 158 263 375 62 118 997 682 qq ò 엄 ò 엄 ò d à ò g ò qq  $\ddot{\delta}$ g g δ

1539 Q-YFQSAIWSGFIKVKKSDEYTFAISADNHVTMWVDD------QEVINKASNSNK---- 105 KQENRLLNESESSSQGLLGY-YPSDLNFQ--APMVVTSSTTGDLSIP--SSELENIPSEN DK----RFHYDRNNI-----AVGADESVVKEAHREVINSSTEGLLINIDKDIRKILSGYI SireAnsalor, MEDLINE=22255705; PubMed=12368864; Mitte O., Berriman M., Hyman R.W., Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlon J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angliuoli S., Pertera M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A. B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., "Genome sequence of the human malaria parasite Plasmodium 548 TEPDFNFDQQTSQNI-----KNQLA-----ELNATNIYTVLDKIKLNAKMNILIR 644 VEIEDTEGLKEVIN--DRYDMLNISSLRODGKTFIDFKK-YND--KLPLYISNPNYKV--510 -PSDPLETTKPDMTL-----XEALKIA----FGFNEPNG------NLOYQGKDI 430 TPITMMYN-----QFLELEKTK-----QLRLDTDQVYGNIATVN-FENGRVRVDTGSNW |:|:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | | |:| | |:| | |:| | | | |:| | | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | |:| | 478 SEVLPQIQETTARIIFN------GKDLNLVERRIAAVN--------Length 2849; Plasmodium falciparum (isolate 3D7). Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. NCBI_TaxID=36329; falciparum.";
Nature 419:498-511(2002).
BmBL; AE014841; AAN35975.1; -.
Hypoth Atloal protein.
SEQUENCE 2849 AA; 335916 MW; B5515D173D96B813 CRC64; Indels Created)
Last sequence update)
Last annotation update) 1591 SWINIFSFEDIFNYLMTYTSPTKGNNNNNDNNNNS 1627 717 Query Match
5.3%; Score 199.5; DB 5;
Best Local Similarity 20.6%; Pred. No. 0.68;
Matches 170; Conservative 132; Mismatches 335; ---NVYAV-----TKENTIINPSENGDIS 2849 AA 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Hypothetical protein. PRELIMINARY; FROM N.A.

1922 EDIIQERFSHNNİKTYEMNKNCSYDSCDNİVKINYDELNDSTQTKELNEGKSNNGKAEAW 1981	106 -IRLEKGRIY-QIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNS 163 	164 RKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSP 223   :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :     :       :       :         :	224 EKWSTASDDYSDFEKVTGRI-DKNVSPEARHPLVAAYPIVHVDMENIILS 272 :	273 KNEDOSTONTDSETRIISKNISTSRTHISEV-HGNAEVHASFFDIGGSVSAG-FSNSNSS 330        :   :   :   :   :   :   :   :	331 TVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVL 378 	379 PITSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIALNAQKDFSSTPITM 434 2222 LINNVILNQNNANNLENLNTNTIGSVQPFVTCPDFYANNIKSIYLDPNLQ 2271	435 NYNQFLELEKTKQLRLDTDQVYGNIATYNPENGRVRVDTGSN 476		529 IAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTV 577 2388 ITNSLHNNNNNNNNNLGGDVLNNSYLFNINSFNPNNAYIYNNNNNNNNNNNNNNNCINYNL 2447	578 LDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLAID 632 2448 LDKKEINVKNEEINWNSVLEDTNKENEGND	633 KDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNP 692 2497 NNIDIISNGQNINNTNANTWKEKRNNNLRDDDIYKKNMKRSNSLDFKKLDSEKK 2550	693 NYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYE 733 	18 SRJN9 PRELIMINARY; PRT; 1404 AA.  QBRJN9; QBRJN9; OTTEMBLE: 21, Created) 01-JUN-2002 (TrEMBLE: 21, Last sequence update) 01-MAR-2003 (TrEMBLE: 23, Last annotation update) 01-MAR-2003 (TrEMBLE: 23, Last annotation update) Wariable membrane protein precursor. WMP. Mycoplasma hominis. Mycoplasma hominis. Mycoplasmaceae; Mycoplasma.
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MOBIL TAXID=2098;
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-132;
Boesen T.;
"Gene and Protein Structure of the Mycoplasma hominis Vaa adhesin.";
Thesis (2001), Department of Department of Medical Microbiology and.
EMBL, AJ416752; CAC95143.1; -.
InterPro; IPR006864; LMP.
Pfam; PF04778; LMP; 3.
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1 24 POTENTIAL. 25 1404 VARIABLE MEMBRANE PROTEIN. 1404 AA; 160137 MW; 2C03F666B3473CAB CRC64;	Similarity 19.7%; Pred. No. 0.5; Similarity 19.7%; Pred. No. 0.5; 8; Conservative 124; Mismatches 282; Indels 240; Gaps 34;	SSELENIPSENOYFOSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVIN 98	KASNSNKIRLEK-GRLYQIKIQYQRENPTEKGLDFKLYWTDSON 141	KKEVI-SSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKN 19	KLBAFNATKKLBFTKLOETRSNIDKFLTPEVKANPNYTTLVNELEVAK	KRTFLSPMISNIHEKKGLTKYKSS-PEKWSTASDPYSDFEKVTG	4 DKAVSPEARHPLVAAYPIVHVDMENIILSKABDQSTQNTDSETRIISKATSTSR 297    :  :  :  :  :  :  :  :  :  :  :  :	DANDI DEDGELYKANALAND.  1 HTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWA	O	<b>ω</b> .	0 1165SONGSDIIGINGTAKAKAKANATIANGATAKAKAATALMAQKDFSSTPITMYYNQFLELEK 44	0 GEIQQAKAELTNEIEKANQTIASNNTALMENSNTSLLNKISEVQNKLDKFNNDKKAEFNK 739	5 TRQLRLDTD	9 EVLPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDWTLKEALKI 52	DALNELÇAKMABİHKKTFQEFNEHKNBLENLIKKEDAKEVGTDEANTAITNNDVKENSSI 85	0 AFGFNEFNGNLQYQGXDITEFDFNFDQOTSONIKNQLA-ELNATNYYTULDKIKLNA 585 0	S KMNILI-	7 KINNLITSSSNQVSAEEISKAKKVLEEINNLSLNNDSSIKSLKEATQKIKDAETQ-LTKE 955	1 IDKDIRKILSGYIVEIEDTEGLKEVINDRYDML 663	6 IEKAKIEKTDKLKKFNBVKKSLEDLIKDDDAIQVGTDDAPKLLEDNNNINE-NSSIEET.	4	S NATKTLEDGKSKLDKKIKTKKQPL 1038	completed: May 3, 2004, 19:39:56 le : 39.6261 secs
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May 3, 2004, 19:26:27; Search time 49.1208 Seconds (without alignments) 4227.791 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM protein - protein search, using sw model Run on:

US-09-848-909A-10 3774 1 EVKQENRLINESESSSQGLL......TSTNGIKKILIFSKKGYEIG 735 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Sequence:

Scoring table:

1586107 segs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2003ss:*

7: geneseqp2003bs:*

8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Anthrax P	Anthrax P	Anthrax P	Anthrax P	Modified	ă	B. anthra	Bacillus	Bacillus	Bacillus	Bacillus	g	C. botuli	C. botuli	C. botuli	C. botuli	Clostridi	Bacillus	MIS toxin	B. cereus
Aam51498	Aam52113	Aam51497	Aam51496	Aar60193	Aae18288	Aay56961	Aae18285	Aae18287	Aae18286	Aae18284	Aam50707	Aae07903	Aae07901	Aae07900	Aae07902	Aae35719	Aaw60224	Aay59277	Aar91239
					-														
AAM51498	AAM52113	AAM51497	AAM51496	AAR60193	AAE18288	AAY56961	AAE18285	AAE18287	AAE18286	AAE18284	AAM50707	AAE07903	AAE07901	AAE07900	AAE07902.	AAE35719	AAW60224	AAY59277	AAR91239
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26	27	28	29	30	31	32	33	34	35	36	37	8	39	40	41	42	43	44	4.5

## ALIGNMENTS

RESULT 1 AAM51493

AAM51493 standard; protein; 735 AA

AAM51493;

01-FEB-2002 (first entry)

Anthrax PA mutant K397D/D425K.

Anthrax, PA, protective antigen, antibacterial, pore-forming toxin; B moiety, A-B anthrax toxin, Bacillus anthracis; vaccine; mutant; mutein.

Bacillus anthracis. Synthetic.

/note= "Wild-type Lys substituted by Asp" Location/Qualifiers Misc-difference 397

Misc-difference 425 /note= "Wild-type Asp substituted by Lys"

WO200182788-A2.

08-NOV-2001

04-MAY-2001; 2001WO-US014372.

04-MAY-2000; 2000US-0201800P.

(HARD ) HARVARD COLLEGE

Sellman BR;

Collier RJ,

WPI; 2002-017725/02.

Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis. 

Claim 4; Page; 77pp; English.

The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1484-AAMS1500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not

mutein

mutant;

anthracis; vaccine;

toxin; Bacillus

anthrax

A-B

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/note= "Wild-type Lys substituted

RJ,

Location/Qualifiers 397

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04-MAY-2000; 2000US-0201800P
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                  Bacillus anthracis
                                                       Misc-difference
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                            Synthetic.
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                                                                                                  EVKQENRLLNESESSSQGLLGYYFSDLNFQAPWVTSSTTGDLSIPSSELENIPSENQYF
                                                                                                                          QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                    QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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 given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                              Length 735
                                             Score 3774; DB 5;
Pred. No. 4.3e-241;
Mismatches 0;
                                              100.0%; Sc
Local Similarity 100.0%; Pous 735; Conservative 0;
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                                                                                                                                   The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM2113 and AAM51844-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus anthracis.
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99.8%; Score 3768; DB 5;
Best Local Similarity 99.9%; Pred. No. 1.1e-240;
Matches 734; Conservative 0; Mismatches 1;
                                                                                                      Claim 4; Page; 77pp; English
                                                                                                                                                                                                                                                                                                                                     Sequence 735 AA;
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PA; protective antigen; antibacterial; pore-forming toxin;

Anthrax PA mutant K397D.

Anthrax;

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protein;

AAM51485 standard;

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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM5113 and AAM51484-AAM5150), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483) 900 009 9 9 720 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKYNVYAVTKENTIINPSENGDTSTNG 720 480 540 540 Anthrax; PA; protective antigen; antibacterial; pore-forming toxin; B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; mutant; mutein. LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY DMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL Lys" ρχ /note= "Wild-type Asp substituted Location/Qualifiers Ą AAM51491 standard; protein; 735 04-MAY-2001; 2001WO-US014372 04-MAY-2000; 2000US-0201800P Claim 4; Page; 77pp; English IKKILIFSKKGYEIG 735 (first entry) Collier RJ, Sellman BR; Anthrax PA mutant D425K. (HARD ) HARVARD COLLEGE WPI; 2002-017725/02 Bacillus anthracis. Synthetic. Key Misc-difference WO200182788-A2 01-FEB-2002 08-NOV-2001 AAM51491; 721 601 199 421 481 541 601 661 721 481 541 RESULT 3 AAM51491 ઠે 음 장 원 상 원 8 q  $\stackrel{>}{\circ}$ Q

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Pred. No. 1.2e-240;
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Sequence 735 AA;

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Bacillus anthracis

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Pred. No. 1.5e-240;
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                                                                   note= "Wild-type Asp
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Matches 734; Conservative
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM5184-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAM51483)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               661 DMLNISSLRQDGKTFIDFKKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG
LNAQKDASSTPITMNYNQFLELEKTKQLRLDTDGOVQGNIATYNPENGRVRVDTGSNWSEV
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                                                                                  LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNBPNGNL
                                                                                                                                 LPQIQETTARIIFNGKDLNLVBRRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                                                                                                                                                                                         QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
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                                                                                                                                                                                                                                                                                                                                                                        Anthrax, PA, protective antigen, antibacterial, pore-forming toxin
B moiety, A-B anthrax toxin, Bacillus anthracis, vaccine, mutant,
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Pred. No. 2.3e-240;
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1844-AAMS1800), especially mutants in the B molety of the pore-forming binary A-B anthrax toxin, where the B molety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is desived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                             "Wild-type Lys substituted
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Pred. No. 2.7e-240;
0; Mismatches 2;
                                Location/Qualifiers 397
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                                                                                                                                            2001WO-US014372.
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ilarity 99.7%;
Conservative
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                                                                                                                                                                             DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG
          LPQIQETTARIIFNGKDLNIVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                481 LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL
                                                          541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKNNILIRDKRFHYDR
                                                                             OYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMYILIRDKRFHYDR
                                                                                                         NNI AVGADESVVKEAHREVINSSTEGLILINI DKDIRKI LSGYIVE I EDTEGLKEVINDRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Wild-type Asp substituted by Asn"
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Length 735;
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99.7%; Score 3762; DB 5;
99.7%; Pred. No. 2.7e-240;
iive 0; Mismatches 2;
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAM52113 and AAM51804-AAM51500), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. The present sequence is that of the anthrax PA protein
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                                                                                                                                         BUKQENRILLNESESSSQGLLGYYFSDLNFQAPWVTTSSTTGDLSIPSSELENIPSENQYF
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                    DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINDSENGDTSTNG
QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR
                                                            NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY
                                                                                                                                                                                                                                                                                                                                                                                                                         Anthrax; PA; protective antigen; antibacterial; pore-forming toxin; B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine.
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Pred. No. 3.1e-240;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                               The sequence encoding the protective antigen of Bacillus anthracis may be used in the construction of a nucleic acid which encodes a fusion protein comprising the anthrax protective antigen binding domain of the native anthrax lethal factor and a sequence encoding an activity inducing domain of a second protein. The fusion proteins are useful for the specific killing of tumour cells or the killing of cells infected with intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to correct PN field.)
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    useful for
tumour cells or

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killing 1
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Pred. No. 3.1e-240;
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                                                                                                                                                                                                                                                             Nucleic acid encoding anthrax toxin fusion targetting toxin to specific cells, eg for
                                                                                                                                                                                     Singh Y,
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                                                                                                                                                                                     Arora N,
                                                                                                                                                        DEPT HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.7%;
Local Similarity 99.7%;
les 733; Conservative (
                                                                                                         93US-00021601
93US-00082849
                                                                           94WO-US001624
                                                                                                                                                                                      Klimpel K,
                                                                                                                                                                                                                   WPI; 1994-279753/34.
                                                                                                                                                                                                                                     N-PSDB; AAQ70180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 735 AA;
                                                                                                                                                                                                                                                                                                  infected cells.
                                                                           14-FEB-1994;
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25-JUN-1993;
                WO9418332-A2
                                               18-AUG-1994
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                                           QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN 180
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                                                                                                                     DGIPDSLEVEGYTVDVRNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
121 QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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Misc-difference 425
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The invention relates to antibacterial agents comprising mutant forms of pore-forming toxins (AAMS2113 and AAMS1800), especially mutants in the B moiety of the pore-forming binary A-B anthrax toxin, where the B moiety is anthrax protective antigen (PA) and using these mutants or compositions of them for protecting against Bacillus anthracis infections in humans, especially as vaccines. Note: The present sequence is not given in the specification but is derived from the Bacillus anthracis wild-type PA protein sequence shown in figure 13 (AAMS1483)
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                                                                                                                                                                             Protecting humans against anthrax using mutant B groups (anthrax protective antigens) of the pore-forming binary A-B toxin of Bacillus
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                   04-MAY-2000; 2000US-0201800P.
                                                                                                                                                                                                                                                            Claim 4; Page; 77pp; English.
                                                         (HARD ) HARVARD COLLEGE
                                                                                                  Sellman BR;
                                                                                                                                        WPI; 2002-017725/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 735 AA;
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SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL

GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT

LNAQKKESSTPITMNYNQFLELEKTKQLKLDTDQVYGNIATYNFENGRVRVDTGSNWSEV

INAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV

NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA

180 240 240

DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGI PDSLEVEGYTVDVKNKRTFLSPWI SNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT

QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN

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QSAIWSGFIKVKKSDEYTFATSADNHVTMMVDDQEVINKASNSNKIRLEKGRLYQIKIQY

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QYQGKDITEFPFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDR

LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL

420 420 720

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Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA; tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial ġ AAY56959 standard; protein; 736 IKKILIFSKKGYBIG 735 IKKILIFSKKGYEIG 735 B. anthracis MAT-PA protein. Bacillus anthracis. WO200002522-A2. 20-JAN-2000 25-APR-2000 661 721 721 AAY56959 

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10-JUL-1998;

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Gaps ., 0

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Score 3761; DB 5; Pred. No. 3.1e-240; 0; Mismatches 2;

Query Match Best Local Similarity 99.7%; Matches 733; Conservative (

Length 735; Indels 9

EVKOENRILNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF

The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus anthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals replaced with those of tissue plasminogen with its secretory signals replaced with those of tissue plasminogen activactor) and PAG3 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing inflectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthracis MAT-PA protein. vaccines for anthrax, in producing and agents inhibiting anthrax. US MEDICAL RES INST INFECTIOUS DISEASES. Smith JF, DNA construct useful as for analyzing the drugs a Disclosure, Page 34; 35pp; English Parker MD, WPI; 2000-182165/16. N-PSDB; AAZS6875. Pushko P, Sequence 736 AA; cells for Recombinant (USME-) Lee JS, host 

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240 241 120 300 360 420 480 481 541 121 181 301 361 421 NNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660 9 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 61 DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHERKGLTKYKSSPEKWSTASDPYSDFEKVT GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAİWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN QRENPTEKGLDFKLYFTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT SEVHGNAEVHASPFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA LNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL QYQGKDITEFDFNFDQQTSQNIKNQLABLNATNIYTVLDKIKLNAKMNILIRDKRFHYDR Gaps ; 0 Length 736; Indels .. N Score 3761; DB 3; Pred. No. 3.1e-240; 0; Mismatches 2; Query Match
Best Local Similarity 99.7%;
Matches 733; Conservative ( ч 62 121 122 181 182 242 301 361 362 422 481 541 601 241 302 421 482 임 ò d à ద à S à g ò qq ð 셤 à g  $\delta$ 엄 Š ò

The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus anthracis proteins, selected from protective antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA with its secretory signals replaced with those of tissue plasminogen activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthracis TPA-PA proteins. The present sequence represents a B. anthracis proteins. 120 148 720 661 88 Recombinant DNA construct useful as vaccines for anthrax, in producing host cells for analyzing the drugs and agents inhibiting anthrax. EVKQENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 1 EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDISTNG QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY protein, protective antigen, PA, MAT-PA, TPA-PA, activator, PA63; vaccine; anthrax; antibacterial ö Length 763; Indels SL; Welkos Match 99.7%; Score 3761; DB 3; Local Similarity 99.7%; Pred. No. 3.3e-240; les 733; Conservative 0; Mismatches 2; (USME-) US MEDICAL RES INST INFECTIOUS DISEASES Smith JF, Ą. Disclosure; Page 32; 35pp; English. protein; 763 Parker MD, 99WO-US015568. 98US-0092416P. IKKILIFSKKGYEIG 735 B. anthracis TPA-PA protein. (first entry) IKKILIFSKKGYEIG WPI; 2000-182165/16. N-PSDB; AAZ56876. Bacillus anthracis tissue plasminogen Pushko P, standard; Bacillus anthracis. Sequence 763 AA; 09-JUL-1999; 25-APR-2000 20-JAN-2000 602 662 721 722 AAY56960; Query Match 53 61 89 661 AAY56960 Lee JS, d ò d à 셤 à 음 8 ò

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                                                    DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
                                                                                                                 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL
                                                                                                                                      NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIA
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                    QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                        DGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVT
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         ORENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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The invention provides a recombinant DNA construct that comprises a vector and at least one nucleic acid (or its fragment) encoding a combination of Bacillus arthracis proteins, selected from protective antigen (PA). MAT-PA (PA with its secretors ignals removed). TPA-PA (PA with its secretory aignals replaced with those of tissue plasminogen activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine for anthrax and in producing infectious alpha virus particles. These particles, expressing the B. anthracis proteins are useful also as vaccines for anthrax. Host cells transformed with the construct are useful for analyzing the effectiveness of drugs and agents that inhibit anthrax or B. anthracis proteins. The present sequence represents a B. anthracis PA protein
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                                                          Recombinant DNA construct useful as vaccines for anthrax, in producing host cells for analyzing the drugs and agents inhibiting anthrax.
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99.7%; Score 3761; DB 3; Length 7

Best Local Similarity 99.7%; Pred. No. 3.3e-240;

Matches 733; Conservative 0; Mismatches 2; Indels
                                                                                                                        Disclosure; Page 33; 35pp; English
WPI; 2000-182165/16.
N-PSDB; AAZ56874.
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This sequence shows the B. anthracis protective antigen (PA). An immunogenic fragment of PA, pCPA, can be used to produce an immune response which protects an animal against lethal injection with Bacillus anthracis. DNA encoding the B. anthracis PA can be used in conjunction with DNA encoding the lethal factor (LF) in a DNA vaccine. Using a DNA vaccine which encodes the muteated LF protein or fragment alone or in combination with a DNA encoding the PA protein or its fragment, both components (humoral and cell-mediated) of the immune system are stimulated, which results in longer term immune memory response. The combined use of a mutated LF and PA gene or their fragments results in a higher level of immune response, as judged by overall serum antibody titers for LF and PA antigens, than the use of either LF or PA genes in
                                                                                                                                                                                                                                               Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine; humoral; cell-mediated; immune memory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protecting animal against lethal infection with Bacillus anthracis, by administering wildtype or mutated form of Bacillus anthracis lethal factor protein or its fragment or a nucleic acid encoding the mutated protein.
                                                                                                                                                                                                                                                                                                                                      1...29
/label= Signal peptide
/lote= "Not given in the specification"
30...764
/label= PA
/label= pCPA
                                                                                                                                                                                                                      Wild type B. anthracis protective antigen
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                                                                                                                               AAB47306 standard; protein; 764 AA
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(GALL/) GALLOWAY D R.
(MATE/) MATECZUN A J.
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N-PSDB; AAC86016.
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Length 764;

Score 3761; DB 4; Pred. No. 3.3e-240;

99.7%;

Query Match Best Local Similarity

Sequence 764 AA

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                                        EVKQENRLINESESSSQGLLGYYFSDINFQAPMVVTSSTTGDLSIPSSELENIPSENQYF 89
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Best Local Similarity 99.7%; Pred. No. 1.2e-254;
Matches 733; Conservative 0; Mismatches 2; Indels
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; MOLECULE TYPE: protein
US-08-021-601-4
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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J Sequence 4, Application US/08021601

J Ratent No. 5591631

J RAPPLICANT: Lippla, Stephen H.
APPLICANT: Rinnel, Kurt R.
APPLICANT: Nichols, Peter J.
APPLICANT: Nichols, Peter J.
APPLICANT: Aligh, Yogendra
TITLE OF INVENTION: RELATED METHODS

UNDERSON ENCURNES: 12
CORRESPONDENCE ADDRESS: 12
COUNTRY: ALLAR A

STREET: 133 Carnedle & Rosenberg, P.C.
STATE: Georgia
COUNTRY: ALLAR BEADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Compatible
OPERATING SYSTEM: PC COMPATION:
MEDICATION NUMBER: US/08/021,601
FILING DATE: 1993021

CLASSIFICATION NUMBER: 144.057
TELEPAN: APPLICATION NUMBER: 144.057
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-JUN-1993
CLASSIFICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber: Kenneth A.
REGISTRATION NUMBER: 15.280-161-1
FELEPHONE: Kenneth A.
REGISTRATION NUMBER: 15.77
REFERENCE/DOCKET NUMBER: 15.70
TELEPHONE: (415) 5.76-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 735 amino acid
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99.7%; Score 3761; DB 1;
Best Local Similarity 99.7%; Pred. No. 1.2e-254;
Matches 733; Conservative 0; Mismatches 2;
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            EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                   QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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APPLICANT: Klimpel, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins of TITLE OF INVENTION: Related Methods
YOMBRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco STATE: California COUNTRY: USA ZIP: 94111-3834 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08082849B Patent No. 5677274 GENERAL INFORMATION:
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241 GRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT
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; Sequence 12, Splication US/08021601
; Patent No. 5591631
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
APPLICANT: Michols, Peter J.
APPLICANT: Aroza, Naveen
; APPLICANT: Singl, Yogendra
TITLE OF INVENTION: ARLARD METHODS
TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: Needle & Rosenberg, P.C.
STREET: 133 Carnegie Way, Suite 400
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: USA

ZIP: 3303

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,601

FILING DATE: 19930212

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Sprart Gwendolyn D.

REGISTRATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414.057

TELEPHONINICATION: IFORMATION:

TELEPHONINICATION: 1FORMATION:

TELEPHONINICATION: A04/688-0770

TELEFRAX: 404/688-9880
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                                 661 DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
DMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
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                                                                                                                                                                                                                  Sequence 4, Application PC/TUS9401624

Sequence 4, Application PC/TUS9401624

GENERAL INFORMATION:

APPLICANT: Klimpel, Kurt R.

APPLICANT: Klimpel, Kurt R.

APPLICANT: Singh, Yogendra

APPLICANT: Nichols, Peter J.

TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS

NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Steuart Street Tower, 20th Floor, One Market
STREET: Place

COUNTRY: USA

ZIP: 94105

CONDUTER: EMA PC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FADDLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Law PAPLICATION DATA:

APPLICATION NUMBER: 15280-115

TILING DATE: June 25, 1993

CLASSIFICATION: NUMBER: 15280-115

TELEPHONE: (415) 543-5043

INPORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 735 amino acids

TYPE: Anio acids

TYPE: Anio acids

TYPE: Anio acids

TYPE: Anio acids
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99.7%; Score 3761; DB 5; Length 735;
Best Local Similarity 99.7%; Pred. No. 1.2e-254;
Matches 733; Conservative 0; Mismatches 2; Indels
                                                                                                                        721 IKKILIFSKKGYEIG 735
                                                                                     721 IKKILIFSKKGYEIG 735
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MOLECULE TYPE: protein
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Fusion Proteins

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COMPUTER READBLE FORM:

COMPUTER READBLE FORM:

MEDIUM TYPE: FIDEPOY disk

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

COMPUTER: ISM FC compatible

APPLICATION NUMBER: US/08/082,849B

FILING DATE: 25-UN-1993

CLASSIPTCATION DATA:

PRIOR APPLICATION NUMBER: US 08/021,601

FILING DATE: 12-FEB-1993

ATTORNEY,AGENT INFORMATION:
                                                                     NUMBER OF SEGURNCES: 35
CORRESPONDENCE ADDRESS:
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
CITY: San Francisco
COUNTRY: USA
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
ITLE OF INVENTION: Anthrax Toxin F.
ITLE OF INVENTION: Related Methods
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                                                                                                                                                     DB 1; Length 903;
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                                                                                                                                                   Query Match 98.5%; Score 3716.5; DB Best Local Similarity 98.9%; Pred. No. 2e-251; Matches 726; Conservative 1; Mismatches 4
 INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                         Score 3716.5; DB 1;
Pred. No. 2e-251;
1; Mismatches 4;
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
RELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 amino acids
                                                                                                                                                                                                                                                                       98.5%;
ilarity 98.9%;
Conservative
                                                                                                                                                          : 903 amino acids amino acid
                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                     linear
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Best Local Similarity
Matches 726; Conserv
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Sequence 12, Application US/08082849B Patent No. 5677274 GENERAL INFORMATION: APPLICANT: Leppla, Stephen H. APPLICANT: Klimpel, Kurt R. APPLICANT: Arora, Naveen

US-08-082-849B-12

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us-09-848-909a-10.rai

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301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARL 360
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APPLICANT: Klimpel, Kurt R.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Nathols, Peter J.
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31, Application US/08082849B; Patent No. 5677274; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                          LPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNL 540
LNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEV 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Arora, Naveen
APPLICANT: Arora, Naveen
APPLICANT: Arora, Naveen
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE 31
CORRESPONDENCE 31
STREET: Steet TOWNSEND KHOURIE and CREW
STREET: Plaza
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98.5%; Score 3716.5; DB 5; Length
Best Local Similarity 98.9%; Pred. No. 2e-251;
Matches 726; Conservative 1; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk COMPUTER: IEM PC Compatible COMPUTER: IEM PC Compatible COMPUTER: DEAD FOR COMPUTER: PLEATION DATA:

SOFTWARE: PATENTIAN ON THE PETTING APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLEASTRICATION:

ATTORNEY/AGENT INFORMATION:

NAME: WEBET COMPUTER: 31,677
REFERENCE/DOCKET NUMBER: 15280-115
TELECOMMUTCATION INFORMATION:

TELECOMMUTCATION INFORMATION:

TELEFAX: (415) 543-9600
TELEFAX: (415) 543-5043
INPORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application PC/TUS9401624 GENERAL INFORMATION:
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amino acid
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STATE: CA
COUNTRY: USA
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TOPOLOGY:
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121 ORENPTEKGLDFKLYWTDSQNKKEVISSDNLOLPELKOKSSNS----RKKRSTSAGPTVP 176
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NDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDT
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                                   24;
                                                                                                                                                                                               Sequence 31, Application PC/TUS9401624

Sequence 31, Application PC/TUS9401624

GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Alimpel, Kurt R.
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Singh, Yogendra
APPLICANT: Stelar BOTHERAY TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Stelart Street Tower, 20th Floor, One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
95.0%; Score 3584; DB 5;
Best Local Similarity 95.3%; Pred. No. 2.6e-242;
Matches 704; Conservative 4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REPERENCE/DOCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
                                                                                                             717 STNGIKKILIFSKKGYEIG 735
                                                                                                                                                               STNGIKKILIFSKKGYEIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-9603
INFORMATION FOR SEO ID NO: 31
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                719 amino acids
amino acid
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MOLECULE TYPE:
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PCT-US94-01624-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 EKVIGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297 RTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIHISEVHGNAEVHASFPDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNL 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WSEVLPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 NGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMILIRDKRF 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVI 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 DRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLIKYKSSPEKWSTASDPYSDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSAIWSGFIKVKKSDEYTFATSADNHVTWWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNTATIMMQRGNFLQGPTVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

95.0%; Score 3584; DB 1;

Best Local Similarity 95.3%; Pred. No. 2.6e-242;

Matches 704; Conservative 4; Mismatches 7;
                                                                                                 APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-UN-1993
CLASSIFICATION: 514
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FBB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 15280-161-1
TELECOMOUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 31:
SEGUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 15280-161-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 719 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-082-849B-31
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RESULT 10
US-08-560-780-32
US-08-560-780-32
Fatent No. 6204435
FAPLICANT: Feiteleon, Jerald S.
APPLICANT: Schmepf, H. Ernest
APPLICANT: Schmepf, H. Ernest
APPLICANT: Schmepf, H. Ernest
APPLICANT: Schmepf, H. Ernest
APPLICANT: Schmepf, James
APPLICANT: Schmepf, James
APPLICANT: Schmepf, James
APPLICANT: Multer-Cohn, Judy
APPLICANT: Multer-Cohn, Judy
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APPLICANT: Multer-Cohn, Judy
APPLICANT: Schmepf, Judy
CONTRESS Saliwanchik, Lloyd & Saliwanchik
ADDRESSERS: Saliwanchik, Lloyd & Saliwanchik
APPLICATION NUMBER: US/08/960,780
FILING DATE: 30-05/1997
ATTONNEY/ASSTITION DATA:
APPLICATION NUMBER: 31,794
RESTRACES AND NUMBER: 31,794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 QENRILINESESSAGGILGYYFSDINFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                        209 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
                   666 SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKIL
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Best Local Similarity 30.2%; Pred. No. 7.2e-46;
Matches 244; Conservative 134; Mismatches 299; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 32: SEQUENCE: CHARACTER STICS: EXQUENCE: CHARACTER STICS: LENGTH: 881 amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE: 177C8
                                                                                                                                             726 IFSKKGYEIG 735
                                                                                                                                                                                                         269 IFSKKGYEIG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-08-960-780-32
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US-09-273-839A-8

Sequence 8, Application US/09273839A

Sequence 8, Application US/09273839A

SEQUENCE 9, Application US/09273839A

SENERAL INVERMATION:
APPLICANT: Cirino, Nick M

APPLICANT: Cirino, Nick M

APPLICANT: Lehnert, Bruce E

TITLE OF INVENTION: Beceptors

TITLE OF INVENTION: Receptors

FILE REFERENCE: S-89,662

CURRENT APPLICATION NUMBER: US/09/273,839A

CURRENT FILING DATE: 1999-03-22

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENTH: 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 NDRYDMINISSIRQDGKTFIDFKKYNDKIPLYISNPNYKNNVYAVTKENTIINPSENGDT 716
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                                                                                                                                                              301 RTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTAD 360
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                                       241 EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNIDSETRTISKNTSTS 300
                                                                                                                                                                                                                                                357 TARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKADENQLSQILAPNNYYPSKNL 416
                                                                                                                                                                                                                                                                                    417 APIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSN 476
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EKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTS 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 VAQE--WGISTGNISQFNIASAGYLNANVRYNNVGTGAIXDVKPTISFVL-NNDTIAIIT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AKSNSTALNISPGESYPKKGONGIAITSMDFNSHPITLNKKOVDNLLNNKPMALETNOT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95 SIRWIGLIQSKETGDFTFNLSEDEQALIEINGKIENKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPEFNKKESQEFLAKPSKINLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OKNQ---QKEMDRKGILGYYFKGKDF-SNLTWFAPTRDSTLIYDQQTANKLLDKKQQEYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 SRKKRSISAGPIVPDRDNDGIPDSLEVEGYIVDVKNKRIFLSPWISNIHEKKGLIKYKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 PEKWSTASDPYSDFEKVTGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKANEDQSTQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 ADENQLSQILAPNNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 SAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 QENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.5%; Score 775; DB 3; Length 881;
Best Local Similarity 30.2%; Pred. No. 7.2e-46;
Matches 244; Conservative 134; Mismatches 299; Indels 130; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RENPTEKGLD-----FKLYMTDSQNKKEVISSDNLQLPBLKQKSS-----
invector: linear

MOLECULE TYPE: peptide

CRIGINAL SOURCE:

INDIVIDUAL ISOLATE: PS177C8

US-09-073-898-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655 VINDRYDMLNI--SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSE 712
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                                                                                                                                                                                                                                                                                            DSETRIISKWISTSRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
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US-00-073-898-32

Sequence 32, Application US/09073898

Patent No. 6242669

CENERAL INPERMATION:

APPLICANT: Schnepf, H. Ernest

APPLICANT: Schneth E.

APPLICANT: Schneth E.

APPLICANT: Schneth E.

APPLICANT: Schneth E.

APPLICANT: Schneth E.

APPLICANT: Downer, David

APPLICANT: Downer, David

APPLICANT: Schneits, James

APPLICANT: Muller-Cohn, Judy

APPLICANT: Muller-Cohn, Judy

APPLICANT: Morrill, George

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APPLICANT: Hostad-Lee, Stacey

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  SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS
                                                                                                                                                                                                      213 QKMKREIDED----TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN
                                                                                                          RENPTEKGLD-----FKLYWTDSQNKKEVISSDNLQLPELKOKSS------
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                                                                                                                                                                                        APPLICANT: Feitelson, Jerald S.
APPLICANT: Schnepf, H. Ernest
APPLICANT: Schnepf, H. Ernest
APPLICANT: Stockhoff, Brian A.
APPLICANT: Stockhoff, Brian A.
APPLICANT: Schwells, James
APPLICANT: Lower, David
APPLICANT: Muller-Cohn, Judy
APPLICANT: Muller-Cohn, Judy
APPLICANT: Finstad-Lee, Stacey
TITLE OF INVENTION: No. 6603063al Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: No. 6603063al Pesticidal Toxins and Nucleotide
TITLE OF INVENTION: Sequences Which Encode These Toxins
NUMBER OF SEQUENCES: 54
                                                                                                                               156 YGNIATYNFENGRVRVDIGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE
                     ---NATNIYTVLDKIKLNAKAMILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                                                       --GLKE
                                                                                                                                                                                                                               655 VINDRYDMINI -- SSIRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSE
                                                       516 TTKPDMTLKEALKIAF--GFNEPNGNLOYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                                                                                                                                         -----LLINID----KDIRKILSGYIVEIEDTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/307,106
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: 841wanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                         713 NGDT-STNGIK---KILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                     764 IKQIYSRYGİKLEDGİLİDKKGĞIHYG 790
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,848
FILING DATE: 30-0CT-1996
PRIOR APPLICATION NUMBER: US 08/960,780
FILING DATE: 30-0CT-1997
PRIOR APPLICATION NUMBER: US 08/960,780
FILING DATE: 0S-WAY-1998
ATTORNEY AGENT INFORMATION:
NAMB: Sanders, Jay M.
REGISTRATION NUMBER: 39,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: FL
COUNTRY: US
ZIP: 32606-669
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDBY disk
COMPUTER: IBM PC COMPARISH
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/09307106
Patent No. 6603063
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 PEKWSTASDPYSDFEKVTGRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 SIRWIGLIQSKETGDFTFNLSEDEQAIIBINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QENRLINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 QKNQ---QKEMDRKGLLGYYFKGKDF-SNLTMFAPTRDSTLIYDQQTANKLLDKKQQEYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 QKMKREIDED---TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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20.5%; Score 775; DB 4; Length 881;
Best Local Similarity 30.2%; Pred. No. 7.2e-46;
Matches 244; Conservative 134; Mismatches 299; Indels 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           713 NGDT-STNGIK---KILIFSKKGYEIG 735
    MA-708C2
REFERENCE/DOCKET NUMBER: MA-7
TELECOMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-375-800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: PS177C8a
                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-307-106-8
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648 KKQYSSNNPDANLTLNTDAQBKLNKNRDYYISLYMKSEKNYQCEITIDGEIYPITTKTVN 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 ADENQLSQILAPNNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
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SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 154
                                                                                                                                                                                                264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         655 VINDRYDMLNI--SSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 PEKWSTASDPYSDPEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRIFLSPWISNIHEKKGLIKYKSS
                                                                                                                                                                                                                                                                                   456 YGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         481 DG---VYKIKDTHGNIVTGGEWNGVIQQIKAKTASIIVDDGE-RVAEKRVAAKDYENPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 TIKPDMILKEALKIAF--GFNEPNGNLOYQGKDITEFDF--NFDQQISQNIKNQLAEL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                                                                             213 QKWKKEIDED----TUTDGDSİPDLWEENGYİI----QNRIAVKWDDSL-ASKGYİKFVSN
                                                                                                                                                                                                                                                                                                                                                     283 DSETRIISKUTSISKIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Warren, Gregory W
APPLICANT: Warren, Michael G
APPLICANT: Wallins, Martha A
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Brian
APPLICANT: Brian
APPLICANT: Carr, Brian
APPLICANT: Carr, Nicholas B
APPLICANT: Estruch, Nicholas B
APPLICANT: Estruch, Nicholas B
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Sequence 6, Application US/08471044

Patent No. 5840868

GENERAL INFORMATION:
APPLICANT: Warren, Marren, Marten A
APPLICANT: Marren, Martha A
APPLICANT: Maye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Carr, Brian
APPLICANT: Carr, Srian
APPLICANT: Carr, Nicholas B
APPLICANT: Estruch, Nicholas B
APPLICANT: Estruch, Nicholas B
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516 TTKPDMTLKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL--
                                                   540 KT-PSLTLKDALKLSYPDEIKEIEGLLYYKNKPIXESSVMTYLDENTAKEVTKQLNDTTG
                                                                                                                                             ---NATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG
                                                                                                                                                                                                                                                                                      627 ------LLLINID-----KDIRKILSGYIVEIEDTE-------GLKE
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COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC compatible
COMPUTER: IN PC COMPATIBLE
COMPATION STATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-UNN-1995
CLASSIFICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
PRIOR APPLICATION NUMBER: US 08/318,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION NUMBER: US 08/037,057
FILING DATE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pacc, Gary M.
REGISTRATION NUMBER: CGC 1695/CIP3/DIV6 - SQLV3
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - TELECOMMUNICATION INCRMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-471-044-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEKWSTASDPYSDFEKVTGRIDKOVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNT 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGNIATYNFENGRVRVDIGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 SIRWIGLIQSKETGDFTFNLSEDEQAIIEINGKIISNKGKEKQVVHLEKGKLVPIKIEYQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 RENPIEKGLD------FKLYWTDSQNKKEVISSDNLQLPELKQKSS------N 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 QKNQ----QKEMDRKGLLGYYFKGKDF-SNLTMFAPTRDSTLIYDQQTAMKLLDKKQQEYQ 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADENOLSQILAPINYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKOLRLDTDQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 20.5%; Score 773; DB 1; Length 884;
Best Local Similarity 30.2%; Pred. No. 1e-45;
Matches 246; Conservative 129; Mismatches 294; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGC 1695/CIP3/DIV7 - SQLv3
       COMPOTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION NUMBER: US 08/218,018
APPLICATION NUMBER: US 08/218,018
APPLICATION NUMBER: US 08/037,057
FILING DATE: 23-MAR-1994
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CJ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 884 amaino acids
"NOD. amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 884 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                      SD--TKFNIDSKTFKELKLFKIDSQNQPQQVQQDELRNPBFNKKESQEFLAKPSKINLFT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 DSETRIISKNISTSRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSS---TVAIDHSLS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              484 DG---VYKIKDTHGNIVTGGEWNGVIQQIKAKTASIIVDDGE-RVAEKRVAAKDYENPED 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 SRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSS 222
                                                                                                                                                                                                                                                                                                                                                                                                                    216 QKMKREIDED----TDTDGDSIPDLWEENGYTI----QNRIAVKWDDSL-ASKGYTKFVSN 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268 PLESHTVGDPYTDYEKAARDLDLSNAKETFNPLVAAFPSVNVSMEKVILSPNENLS--- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NSVESHSTINWSYT----NTE-----GASVEAGIGPKGISFGVSVNYQHSET 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 LAGERTWAETMG----LNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  367 VAQE--WGISTGNISQENIASAGYLNANVRYNNVGTGAIYDVKPTISFVL-NNDIIAIIT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADENOLSQILAPNNYYPSKNLAPIALNAQKDFSSTPITMNYNQFLELEKTKQLRLDTDQV 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIKPDMILKEALKIAF--GFNEPNGNLQYQGKDITEFDF--NFDQQTSQNIKNQLAEL-- 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 ---NATNIYTVLDKIKLNAKMYNLLIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEG 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----GLKE 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      655 VINDRYDMLN------ISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKE 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 QENRILINESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELEN--IPSENQYFQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.5%; Score 773; DB 2; Length 884;
Best Local Similarity 30.2%; Pred. No. 1e-45;
Matches 246; Conservative 129; Mismatches 294; Indels 146; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTIINPSENGDT-STNGIK---KILIFSKKGYEIG 735
; INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 884 amino acids

; TYPE: amino acids

; TYPE: amino acids

; TYPE: protein

US-08-471-044-5
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Search completed: May 3, 2004, 19:42:42 Job time : 17.0986 secs

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May 3, 2004, 19:40:13 ; Search time 36.6393 Seconds (without alignments) 5560.545 Million cell updates/sec
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3774
1 EVKQENRLLNESESSSQGLL......TSTNGIKKILIFSKKGYEIG 735
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1138120 segs, 277189581 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SOMMERTES		Description	Sequence 30, Appl	Sequence 1, Appli	ď	6	4	'n	9	Sequence 7, Appli	8	0,	Sequence 10, Appl	11,	12,	Sequence 13, Appl	Sequence 14, Appl
		CI	US-10-410-647-30	US-09-848-909-1	US-09-848-909-2	US-09-848-909-3	US-09-848-909-4	US-09-848-909-5	US-09-848-909-6	US-09-848-909-7	US-09-848-909-8	US-09-848-909-9	US-09-848-909-10	US-09-848-909-11	US-09-848-909-12	US-09-848-909-13	US-09-848-909-14
			15	12	12	12	12	12	15	12	12	12	12	12	12	12	12
		Match Length DB	735	736	736	736	736	736	736	736	736	736	736	736	736	736	736
	% Ouerv	Match	7.66	99.7	99.7	99.7	99.7	7.66	7.66	99.7	99.7	7.66	99.7	99.7	99.7	99.7	99.7
		Score	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761	3761
	Result	No.	1	C4	m	4,	ß	ω	7	œ	on	10	11	12	13	14	15

Seguence 15, Appl	76	equence 17	78	O/	20	21	23	'n	Sequence 5, Appli	equence 6,	equence 9,	equence 13	equence 13	equence 30	89			_~	Sequence 4, Appli		Ζ.	т.			'n		2	۲,	Sequence 3, Appli
-848-909-1	-09-848-909-	-848-909-1	-09-848-909-1	48-909-1	-09-848-909-2	-09-848-909-2	-09-848-909-2	-10-442-502-	0-442-502	-10-442-502-	-10-402-466A-	0-402-466A-	-10-332-282-1	-09-848-909-3	10-253-286-68	0-245-871-6	9-747-521-	3-10-106-014-	10-105-6	-10-105-69	-09-848-90	-10-332-28	-10-402-46	-10-442-502-	0-33	-10-332-282-	-10-402-46	-332-2	-10-332-282-
12	12	12	12				12	15	15	15	12	12	14	12	12	15	σ	13	13	14	12	14	12	15	14	14	12	14	14
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## ALIGNMENTS

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Sequence 30, Application US/10410647

Bublication No. US20030235818A1

GENERAL INFORMATION:

APPLICANT: BEXUS VACCINE, INC.

APPLICANT: Rarritch, Vsevolod

APPLICANT: Bordner, Andrew

APPLICANT: Bordner, Andrew

APPLICANT: Borner, Andrew

APPLICANT: Borner, Andrew

APPLICANT: Borner, Andrew

APPLICANT: Deans, Robert

ILE REPERBNCE: PLEXI110-1 US/10/410,647

CURRENT APPLICATION WUMBER: US 60/373,668

PRIOR PELICATION NUMBER: US 60/373,668

PRIOR PLING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

PRIOR FILING DATE: 2002-04-08

NUMBER OF SEQ ID NOS: 46

SOFTWARE: PATENTIANT VERSION 3.1

SEQ ID NO 30

LENGTH: 335
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; ORGANISM: Bacillus anthracis
US-10-410-647-30
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241 GRIDKAVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHT 300
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Publication No. US2002003958BA1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: 2000-04-04
CURRENT PILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
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US-09-846-909-1
Sequence 1, Application US/09848909
Sequence 1, Application US/09848909
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Colliar, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
FILE REPERBNCE: 0742/060002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR PLLICATION NUMBER: US 60/201,800
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO :
LENGTHE: The Collian Section 4.0
SEQ ID NO :
LENGTHE: The Collian Section 4.0
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Best Local Similarity 99.7%; Pred. No. 4.3e-272;
Matches 733; Conservative 0; Mismatches 2;
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                                                                                                                                    Length 736;
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                                                                                                                                      Score 3761; DB 12;
Pred. No. 4.3e-272;
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                        Version 4.0
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                                                                                                                                    Match 99.7%;
Local Similarity 99.7%;
les 733; Conservative
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NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows
SEQ ID NO 3
LENGTH: 736
                                                                                          anthracie
                                                                      TYPE: PRT
ORGANISM: Bacillus
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US-09-848-909-4
                                                                                                        US-09-848-909-3
                                                                                                                                        Query Match
Best Local S:
Matches 733
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Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR FILING DATE: 2000-04-04
                                      Length 736,
                                                                        Indels
                                      Score 3761; DB 12;
Pred. No. 4.3e-272;
                                                                        0; Mismatches
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                                                        Best Local Similarity 99.7
Matches 733; Conservative
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US-09-848-909-3
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Sequence 4, Application US/09848909
; Publication No. US20020039588A1
; GENERAL INFORMATION:
    APPLICANT: Collier, R. John
; APPLICANT: Seliman, Brett R.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
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TITLE OF INVENTION: and Prevention of Bacterial Infection FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
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Pred. No. 4.3e-272;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 733; Conservative
                                                                                                                                       TYPE: PRT;
CRGANISM: Bacillus anthracis
US-09-848-909-4
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RESULT 6 US-09-848-909-5

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Sequence 5, Application US/09848909;
Publication No. US20020039588A1
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: And Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 736
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Pred. No. 4.3e-272;
0; Mismatches 2;
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Conservative
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US-09-848-909-5
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Best Local Similarity
Matches 733; Conserv
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                                                                                                                                                                                                                                      Sequence 7, Application US/09848909
; Publication VO US20020039588A1
; GENERAL INFORMATION:
; APPLICANT: COLLIET. R. John
; APPLICANT: CALIMAT, Brett R.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 736;
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                                                                                                                                IKKILIFSKKGYEIG 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bacillus anthracis
US-09-848-909-7
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Best Local Similarity 99.7<sup>3</sup>
Matches 733, Conservative
                                                                                                    IKKILIFSKKGYEIG
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US-09-848-909-7
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Publication No. US202003958BA1
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Publication No. US2020203958BA1
Publication No. US2020203958BA1
Publication No. US2020203958BA1
APPLICANT: Sollman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
CURRENT FILING DATE: 00742/06002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR PILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 736
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Pred. No. 4.3e-272;
0; Mismatches 2;
721 IKKILIFSKKGYEIG 735
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Best Local Similarity 99.7%;
Matches 733; Conservative
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US-09-848-909-6
                                                                              RESULT 7
US-09-848-909-6
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US-09-848-909-9
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Sequence 8, Application US/09848909

Sequence 8, Application WS. US2002039588A1

GENERAL INFORMATION:
APPLICANT: Coller, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT FILING DATE: 2001-05-04
PRIOR PELING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PASSEQ for Windows Version 4.0

LENGTH: 736
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Sequence 11, Application US/08848909

Publication No. US20020039588A1

GENERAL INPORMATION:

APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: and Prevention of Bacterial Infection

TITLE OF INVENTION: and Prevention of Bacterial Infection

TITLE OF INVENTION: and Prevention of Bacterial Infection

TITLE OF INVENTION: and Prevention of Bacterial Infection

CURRENT APPLICATION NUMBER: US/09/848, 909

CURRENT FILING DATE: 2001-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 736
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Best Local Similarity 99.7%;
Matches 733; Conservative
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Publication No. US2002003958BA1

Publication No. US2002003958BA1

Publicant: Collier, W. John

APPLICANT: Sellman, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

TITLE OF INVENTION: and Prevention of Bacterial Infection

TITLE OF INVENTION: UNMBER: US/09/848,909

CURRENT FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-04-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 736
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; ORGANISM: Bacillus anthracis
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; Publication V. US20020039588A1
; Publicartion N. US20020039588A1
; GENERAL INFORMATION:
; APPLICANT: Collier: R. John
; APPLICANT: Collier: R. John
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; TITLE OF INVENTION: And Prevention of Bacterial Infection
; TITLE OF INVENTION: AND PRESENTION OF SECOND (SOF)
; FILE REFERENCE: 00742/66002
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
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.larity 99.7%; Pred. No. 4.3e-272;
Conservative 0; Mismatches 2; Indels 0
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Publication No. US20020039588A1
GENERAL INFORMATION:
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on of Bacterial Infection
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Publication No. US20020039588A1
GENERAL INFORMATION:
TATLE OF INVENTION: Compounds and Methods fo:
TITLE OF INVENTION: and Prevention of Bacte:
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909
CURRENT PAPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
TYPE: FRI
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Score 3761; DB 12;
Pred. No. 4.3e-272;
0; Mismatches 2;
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Sequence:

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Scoring table:

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Sequence 10, Application PC/TUS0335733
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR APPLICATION NUMBER: US 60/424,987
PRIOR APPLICATION NUMBER: US 60/424,987
SOFTWARE: FASEI 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASEI DA NO 10
SEQ ID NO 10
TUBER: PRI
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US-09-848-909A-10

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US-08-848-909A-2

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US-09-848-909A-7

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         ; ORGANISM: Bacillus anthracis
PCT-US03-35733-10
       3, 2004, 19:36:13 ; Search time 175.546 Seconds (without alignments) 4086.665 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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                                                                                                                   QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
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              EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
                                                                 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
                                      EVKQENRLLNESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSENQYF
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GENERAL INFORMATION:
GENERAL INFORMATION:
TOTAL OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection
FILE REFERENCE: 00742/060002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT APPLICATION NUMBER: US 60/201,800
FRIOR PILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 735
TYPE: PRT
CREATER PREVENTION SET OF MINDOWS VERSION 4.0
SEQ ID NO 10
CREATER PREVENTION SET OF MINDOWS VERSION 4.0
CREATER PREVENTION SET OF MINDOWS VERSION 4.0
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Sequence 4, Application PC/TUS0319786
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Modified Shine Dalgarno Sequences and Methods of Use Thereof;
TITLE OF INVENTION: Modified Shine Dalgarno Sequences and Methods of Use Thereof;
CURRENT APPLICATION NOBER: PCT/US03/19786
CURRENT FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
SEQ ID NO 4
IENGTH: 735
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tch 100.0%; Score 3774; DB 23; al Similarity 100.0%; Pred. No. 1.1e-299; 735; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                   1; Indels
                                                                                                                                                                 Length
                                                                                                                                                             Score 3768; DB 1;
Pred. No. 3.3e-299;
0; Mismatches 1;
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 735
TYPE: PRT
ORGANISM: Bacillus anthracis
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APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Me
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                                                                                                                                                                 Query Match
Best Local Similarity 99.9%;
Matches 734; Conservative
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                                         ; OTHER INFORMATION: Mature PA sequence including an ETB signal PCT-US03-19786-4
                                                                                            Length 735;
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/07203
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/424,987
                                                                                                                                Indels
                                                                                            Score 3771; DB 1;
Pred. No. 1.9e-299;
1; Mismatches 0;
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Query Match 99.8%;
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and Prevention of Bacterial Infection
                                                                                                                                                                Score 3768; DB 23;
Pred. No. 3.3e-299;
0; Mismatches 1;
       FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT FILING DATE: 2001-05-04

FRIOR PRILOR PILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 735
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CRGANISM: Bacillus anthracis
US-09-848-909A-2
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RESULT 6 PCT-US03-35733-8

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE PREPARED: 0742/072003
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 735
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llarity 99.9%; Pred. No. 4.8e-299;
Conservative 0; Mismatches 1;
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                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Collier, R. John

APPLICANT: Collier, Brett R.

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

CURRENT APPLICATION NUMBER: US 60/201,800

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8
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Pred. No. 3.9e-299;
0; Mismatches 1;
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Best Local Similarity 99.9%;
Matches 734; Conservative
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RESULT 10
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                                 DMINISSLRODGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNG 720
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Pred. No. 4.8e-299;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                       Sequence 13, Application US/09848909A
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/066002
CURRENT APPLICATION NUMBER: US/09/848,909A
CURRENT APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
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SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 734; Conservative
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US-09-848-909A-13
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(GENERAL INPORMATION:
TITLE OF INVENTION: Compounds and Methods for the Treatment
TITLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/072003
(CURRENT APPLICATION NUMBER: PCT/US03/35733
(CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 05/424,987
(WIMBER OF SEQ ID NOS: 38
(SOFTMARE: PRESER OF SEQ ID NOS: 38
(SOFTMARE: PRESER OF Windows Version 4.0)
(SEQ ID NO 7)
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Local Similarity 99.7%; Pred. No. 8.4e-299;
nes 733; Conservative 1; Mismatches 1;
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PCT-US03-35733-4; Sequence 4, Application PC/TUS0335733; GENERAL INFORMATION:
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                                                                                       541 QYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLMAKMNILIRDKRFHYDR 600
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Sequence 7, Application US/09848909A

Sequence 7, Application US/09848909A

APPLICANT: Collier, R. John

APPLICANT: Collier, R. John

TITLE OF INVENTION: Compounds and Methods for the Treatment

TITLE OF INVENTION: Compounds and Prevention of Bacterial Infection

FILE REFERENCE: 00742/060002

CURRENT APPLICATION NUMBER: US/09/848,909A

PRIOR FILING DATE: 2001-05-04

PRIOR FILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-04

NUMBER OF SEQ ID NOS: 35

SOFTWARE: FastSEQ for Windows Version 4.0
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                                        601 NNIAVGADESVVKEAHREVINSSTEGLILNIDKDIRKILSGYIVEIEDTEGLKEVINDRY 660
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TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: Compounds and Methods for the Treatment TITLE OF INVENTION: and Prevention of Bacterial Infection CURRENT PILE REFERENCE: 00142/072003
CURRENT FILING DATE: 2003-10-10
PRIOR PILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 735
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61 QSAIWSGFIKVKKSDEYTFAŢSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                                        301 SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGINTADTARL 360
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Sequence 4, Application US/09848909A;
GENERAL INFORMATION:
APPLICANT: Collier, R. John
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for the Treatment;
TITLE OF INVENTION: Compounds and Methods for US-00000;
CURRENT PILING DATE: 2001-05-04;
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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GENERAL INFORMATION:
APPLICANT: President and Fellows of Harvard College et al.
ITILE OF INVENTION: Compounds and Methods for the Treatment
ITILE OF INVENTION: Compounds and Methods for the Treatment
ITILE OF INVENTION: and Prevention of Bacterial Infection
CURRENT APPLICATION NUMBER: PCT/US03/35733
CURRENT APPLICATION NUMBER: PCT/US03/35733
FRIOR FILING DATE: 2003-10-10
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NOS
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US-09-848-909A-6
Squence 6, Application US/09848909A
GENERAL INFORMATION:
APPLICANT: Collier, R. John
APPLICANT: Sellman, Brett R.
TILLE OF INVENTION: Compounds and Methods for the Treatment
TILLE OF INVENTION: and Prevention of Bacterial Infection
FILE REFERENCE: 00742/06002
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/201,800
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 735
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Pred. No. 1e-298;
0; Mismatches 2;
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Best Local Similarity 99.7%;
Matches 733; Conservative 0
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May 3, 2004, 19:30:47 ; Search time 13.0855 Seconds (without alignments) 5403.004 Million cell updates/sec Run on:

US-09-848-909A-10 3774 1 EVKQENRLLNBSESSSQGLL......TSINGIKKILIFSKKGYEIG 735 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 78:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

Caccession: 159344. Sigitio; Figoida  Caccession: 159344. Sigitio; Figoida  Aptrices Sequence and Canalysis of the DNA encoding protective antigen of Bacillus Aptrices Sequence and Canalysis of the DNA encoding protective antigen of Bacillus Aptrices Sequence and Canalysis of the DNA encoding protective antigen of Bacillus Aptrices Sequence and Canalysis of the DNA encoding protective antigen of Bacillus Aptrices Sequence T19333, WILD 89172073, PRD:1144491.  Aptrices T0 Cardon, W. M. Leppla, S.H.; Klimpel, K.R.; Birch, N.P.; Loh, Y. Arch. Biochem. Biophys. 316, 5-13, 1995 Aptrices T0 Cardon, W. M.; Leppla, S.H.; Klimpel, K.R.; Birch, N.P.; Loh, Y. Aptrices T0 Cardon, W. M.; Leppla, S.H.; Klimpel, K.R.; Birch, N.P.; Loh, Y. Aptrices T0 Cardon, Signification of Aptrice Drocessing of Anthrax coxin protective antigen by recombinant P. Aptrices To Cardon, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Aptrices To Cardon, R.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Aptrices To Cardon, R.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Aptrices To Cardon, R.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Aptrices To Pallandary Aptrices T0 Cardon, Signification of Exot, the large Bacillus anthracis plasmid Aptrices T0 Cardon, T0 Cardo, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Aptrices T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, Aptrices T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Cardon, T0 Ca
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cryptic protein - Bacillus anthracis
Cryptic protein - Bacillus anthracis
Cryptic protein - Bacillus anthracis
Cryptic protein 1996 #sequence_revision 19-Jul-1996 #text_change 15-Oct-1999
Cryptic 13933
R.Welkos, S.L.; Lowe, J.R.; Eden-McCutchan, F.; Vodkin, M.; Leppla, S.H.; Schmidt, J.J.
Gene 69, 287-300, 1988
Apritie: Sequence and analysis of the DNA encoding protective antigen of Bacillus anthr
A, Reference number: 139933; MUID:89172073; PMID:3148491
A, Accession: 139933
A, Accession: I39933
A, Accession: Light analysis of the GB/EMBL/DDBJ
A, Accession: Light analysis of the GB/EMBL/DDBJ
A, Reference Tests A, Accession: Cryptic DNA
A, Reference Cryptic DNA
A, Cross-references: GB:M22589; NID:g143280; PIDN:AAA22636.1; PID:g143281
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FQSAIWSGFIKVKKSDEYTFATSADNHVTWMVDDQEVINKASNSNKIRLEKGRLYQIKIQ 119
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6.2%; Score 235.5; DB 2; Length 192;
Best Local Similarity 34.6%; Pred. No. 2.6e-05;
Matches 56; Conservative 36; Mismatches 47; Indels 23
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C,Species: Clostridium perfringens
C,Species: Clostridium perfringens
C,Species: 16-40g-1996 #sequence_revision 16-Aug-1996 #text_change 15-Oct-1999
C,Accession: 140862; 842774
R,Perelle, S.; Gibert, M.; Boquet, P.; Popoff, M.R.
Infect. Immun. 61, 5147-5156, 1993
A/Title: Characterization of Clostridium perfringens iota-toxin genes and expression:
A,Accession: 140862
A,Accession: 140862
A,Accession: 140862
A,Besidues: 140862
A,Essidues: 1875 cRES>
A,Cross-references: EMBL:X73562; NID:g929031; PIDN:CAA51960.1; PID:g414655
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        QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY 120
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                             QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQY
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Matches 174; Conservative 132; Mismatches 324; Indels 186; Gaps  19 LLGYYFSDLNFQAPMVYTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYT	DD 3796 WLIKGQIDNIN-PETKYKLENIELSKPLKTHTHILSVSINDKENISLITETGNPVLKV 3851  09 180NDGIPDSLEVEGYTVUVKURTFLSPNISNIHBKKGLTKYKSSPEKMSTASDPYSD 235  1852 IQTQNDTINDTQQTINVTLSGVNSK-YNGRQIKVYKDNNNVIYESSLITLQKGKND 3907  236 FEKYTGRIDDKNVSPEARHPLVAAYPIVHVDNENIILSKN-EDGSTQNIDSET-RTISKNT 293  1:::::::::::::::::::::::::::::::::::	444 KTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNW\$EVLPQIQETTARIIFNGKD 497	Oy 681  Oy 682  Oy 682  Db 4416  RESULT 6  T28676  T28676  T28676  T28676  T28676  T28676  T28676  T387616: Compa  A, Title: Compa  A, Reference mu A, Accession: T A, Status: prel A, Molecule typ A, Residuas: 1-
OY 587 MNILIRDKREHYDRNNIAVGADESVVKEAHREVINSSTECLLLNIDKDIRKILSGYIVEI 646	RESULT 4 G59104 Whypothetical protein pXO1-111 - Bacillus anthracis virulence plasmid pXO1 C.Species: Bacillus anthracis C.Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000 C.Accession: G59104 D. Bacteriol. 181, 6509-6515, 1999 J.Yiltels : Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori A.Reference number: A59091; MUID:99445483; PMID:10515943 A.Accession: G59104 A.Accession: G59104 A.Accession: G59104 A.Accession: G59104 A.Stetiminary A.Molecule type: DNA A.Residues: 1-204 < OKI> A.Residues: 1-204 < OKI> A.Residues: Lenne A.Note: similar to hypothetical protein in the protective antigen domain; ypa, plasmid E.Genome: plasmid A.Genome: plasmid	Query Match         6.2%; Score 235.5; DB 2; Length 204;           Best Local Similarity 34.6%; Pred: No. 2.8e-05;         Action 23; Gaps 6;           Matches 56; Conservative 36; Mismatches 47; Indels 23; Gaps 6;         Action 200           Qy         S87 MNILIRDKEPHYDRNNIAVGADESVVKBAHREVINSTEGLLINIDKDIRKILSGYIVEI 646           Db         1 MNILVRDP-YHYDRNIAVGADESVKRAYKQILNWSSDGVSLNLDEDVNQALSGYMLQI 59           Qy         647 EDTEGLKEVINDRYDMLNISSIRQDGKTFIDFKKYNDKLPLYISNPN 693           Cy         647 EDTE	RESULT 5  RESULT 5  RESULT 5  RESULT 5  RESULT 5  RESULT 5  RESULT 6  RESULT 6  RESULT 6  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT 7  RESULT

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                                                                        #text_change 09-Jun-2000
      Subbus

Subbus

NiAlternate names: gp195 surface antigen

C.Species: Plasmoddium filatparum

C.Species: Plasmoddium falatparum

C.Date: 12-Feb-1993 #equence_revision 12-Feb-1993 #text_change 09-Jun-2000

C.Accession: S05603; S04850

R.Wyler, P.J.

Submitted to the EMBL Data Library, April 1989

A;Reference number: S05603

A;Meccasion: S05603

A;Meccasion: S05603

A;Meccasion: S05603

A;Meccasion: S05603

A;Meccasion: S05603

A;Meccasion: S04850

A;Title: Nuclectide and deduced amino acid sequence of the gp195 (MSA-1) g6

A;Title: Nuclectide and deduced amino acid sequence of the gp195 (MSA-1) g6

A;Reference number: S04850; MUD:89345116; PMID:266887

A;Molecule type: mRNA

A;Residues: 1504-1639 < MYL2>

A;Rosidues: 1504-1639 < MYL2>

A;Rosidues: 1504-1639 < MYL2>

A;Cross-references: EMBL:X15063

C;Superfamily: major merczoite; surface antigen

C;Keywords: glycoprotein; merczoite surface antigen

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-1639/Product: major merczoite surface antigen #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENRL-LNESESSSOGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENOYFQSA
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4.9%; Score 185.5; UB 4;
Best Local Similarity 20.5%; Pred. No. 0.21;
Matches 170; Conservative 138; Mismatches 256;
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                                                                                                                                                                                                                                                                                   43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  875 AYIDDLDNIKKKKSQEI---EKEMNINMDIKMDIHKEMKALNISHDDYKIYHTTSKNHEEK 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIRKILSGYIVEIEDTEGLKE-----VINDRY---DMLNISSLRQDGKTFIDFKKYND 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MENIILSKNEDOSTONTDSETRIISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFS 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NINEIKEKLKDYDFQDFGK------EKNIKYPDEN--KIKNDIDTLNQK 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                PSIEIKIMKDE---FLSKVNKYNDFDKVYKEKVESEHNKFTELTNKIKTEVSDEEIKKYE 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OKSSNSRK--KRSTSAGPTVPDRDNDGIPD-----SLEVEGYTVDVKNKRIFLSP 205
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      PIDN: AAB41263.1
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                                                                                                                                                                                                                                                                                                                            --FOAPMVVTSSTTGDLSI
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A;Cross-references: EMBL:U36927; NID:g1041784; PID:g1041785; PIDN:AAI B;Keen, U; Holder, A.; Playfair, U; Lockyer, M.; Lewis, A. Mol. Biochem. Parasitol. 42.246; 1990.
A;Title: Identification of the gene for a Plasmodium yoelii rhoptry 1 A;Reference number: A48521; MUID:91101660; PMID:2270106
A;Rccesion: A45521
A;Status: preliminary
A;Rolecule type: DNA
A;Redeus: 2260-2401 < KEE>
A;Residues: 2260-2401 < KEE>
                                                                                                                                                                                                                                                                                   221;
                                                                                                                                                                                                                                        Length 2401;
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                                                                                                                                                                                                                        Score 188.5; DB 2;
Pred. No. 0.26;
                                                                                                                                                                                                                                            Ouery Match 5.0%; Score 188.5; E
Best Local Similarity 21.7%; Pred. No. 0.26;
Matches 182; Conservative 119; Mismatches
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Oy 577 VLDKIKLNAKANILIRDKRFHYDRNNIAVG-ADESVVKEAHREVINSSTEGLL 628	RESULT 8 B90598 membrane nuclease, lipoprotein [imported] - Mycoplasma pulmonis (strain UAB CTIP) C;Species: Mycoplasma pulmonis C;Species: Mycoplasma pulmonis C;Date: 24-May-2001 #text_change 03-Aug-2001 C;Accession: B90598 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.; Nucleic Acids Res. 29, 2145-2153, 2001 A,Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm A;Reference number: A99512; MUD:21267165; PMID:11353084 A;Accession: B90598 A;Actuals: Preliminary A,Actuals: Arguinary A,Actuals: Arguinary A,Actuals: Arguinary A,Actuals: Arguinary A,Actuals: Arguinary A,Actuals: Arguinary A,Actuals: Arguinary	A; Residues: 1-1125 < KUR> A; Residues: 1-1125 < KUR> A; Experimental source: gtrain UAB CTIP C; Genetics: C; Genetics: 4:9%; Score 184.5; DB 2; Length 1125; Best Local Similarity 19:1%; Pred. No. 0.13; Matches 165; Conservative 162; Mismatches 330; Indels 207; Gaps 40; Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy Cy	63 AIWSGEIKV	J 47 W 47 44 W RU W RU A A

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OY 286 TRIISKNISTSRIHISEVHGNAEVHASFFDIGGSVSAGFSNSNSSIVAIDHS	QY         383LVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALMAQKDFS 428           D         2828 QAANQVNTNKTALNGAQNLANKKQETTANINRLSHLNTAQKQDL 2871           QY         429 STPITMANN-QFIELEKTKQLRLTDDQV	OY 460 ATYNFENGRVRYDTGSNWSEVLPQIQE-TTARIIFNGKDLNLVERRIAAVNPS	Qy 512 DPLETTKPDMTLKEALKTAFGFNEPNGNLQYQGKDITE		Qy 600 RNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVIN 657	Qy 658 DRYDMINISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTII 708	Oy 709 NPSEN	Db 3192 DQTTN 3196	RESULT 11 T28677 T28677 T28677 T28677 T2967:es: Plasmodium yoelii C;Species: Plasmodium yoelii C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000 C;Accession: T28677; G45521 R;Keen, J; Sinha, K; Brown, K.; Holder, A. Mol. Biochem, Parasitol. 65, 171-177, 1994		A; Molecule Lype: DNA A; Residues: 1-2269 < KRES. A; Cross-references: EMBL: L27838; NID: 9457145; PID: 9457146; PIDN: AAA21304.1 R: Keen. J.; Holder, A.; Playfair, J.; Lockyer, M.; Lewis, A.				OY 1 EVKOENRLLNESESSQC :     :       ::
429 STPITMANNOF		Qy 606 GADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVE 645	YSDNQAGTYYLTSNIKGLFTPKGSQTPQAPGTYSPFNQPLSSLNIYNKGFSSENL KNMYNAVTKENNIINPSENGPTSNIKIIKII 725	1360 KTLLGILSQNSATLKEMIESNQLDNITN-INEVL 13	ESULT 10 89921 ypothetical protein ebhA [imported] - Staphylococcus aureus (strain N315)	~ ~		ancer. Jr. 120 120 120 120 120 120 120 120 120 120	A;Accession: Busyat. A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-6713 <kur> A;Cross-references: GB:BA000018; PID:g13701232; PIDN:BAB42527.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: ebhA</kur>	Query Match Best Local Similarity 20.4%; Pred. No. 2.5; Matches 172; Conservative 125; Mismatches 292; Indels 256; Gaps 43	9MVVTSSTTGDLSIPSSELENIPSENQYPQSA 63 	QY 64 IWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKI 118	QY 119 QYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGP 173	QY 174 TVPDRDNDG1PDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEK 225	QY 226 WSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSE 285 :

A; Cross-references: EMBL: AF057695; NID: 93929017; PID: 93929018; PIDN: AAC79757.1

do do	485 QTKLENKFTEFSLANHEANNNELI-KYFSDLKANLGINEENMLYNQFTEKEKTFNDIKEK 543	a i
٥'n	57 NOYPOSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEK 110	) A
qq	544 NIHINEEISKIEIKIHAS-IYNISERTEREIGINIESLNTKVFEKVKENVTNLNKIK-EK 601	
0,7	111 GRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQ 152	
Db da	602 LKHYDFSDFGKEGNIKYTDKIKKINDDIMAVSQQIDQHINGLDDIQKKSES 652	ð
Oy 1	153 -LPELKQKSSNSRKKRSTSAGPTVPDRDNPGIPDSLEVEGYTVDVKNKRTFLSPWISNIH 211	ă
9 90	653 YVSEMKEQINKLEKVSNTEISNDNVEGIKKKQQIIVTKID 692	6
70	212 BKKGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPL 255	ä
9 40	693 KKKNIYEEINKLLSEISKIEKDNTSLEKVKDINLSYGQNLGNLFLEQIDEE-KKKAENTI 751	8
2	256 VAAYPIVHVDMENIILSKNEDOSTONTDSETRTISKNTSTSRTHTSEVHGNAEVHA 311	ដ
Db 7	752 KSMEAYID-DLDNIKKKSQEIETEMDIKMDINKEMEALKISHDDDKKCHDKSKOHKENIS 810	8
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go qo	811 DIYDKSSKIIQDFSR-ESDINDIKNKLQKNVSESQNHNSDINQCLNEV 857	8
3	372 APIVNVLPTISLVLGKNQTLATIKADENQLSQILAPNNYYPSKNLAPIALNAQK 425	ជ
9 qa	858 ANIYNILKLNKIKKIIDKVKEYTSEIEKNKKNINDELNNSEK 899	8
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δ,	459 IATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDINLVERRIAAVNPSDPLETTK 518	ă
qa	960 IVLSNFNNIEMADNKSQYILEIKKNNGTNDHDYNIKELK-SHKDKSNGYK-TE 1010	Ø
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Db 10	1062 IKDAHNYCTLESGKSEKRANEIKNEKIHIEDEVANNDKSNKAITSIKVSVEPFKTKIIKI 1121	6
δγ.	622SSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLR 669	검
Db 11	1122 NEIRTKSDDCLKETNDLEKQISNLSIDTQETKLTENGKQLKTLEBLLESLK 1172	6
\$ ≿	670 QDGKTFIDFKKXNDKLPLYISNPNYKVNVYAVIKENTIINPSENGDTSTNG 720	검
Db 11	1173 KOKKANIEDQKKELDEVNSKIKNIENTVNQHKKAYEIGIVEKINEIAKTNKAVEISTKE 1230	8
ζ	721 IKK 723	ä
Db 12	1231 LIK 1233	8
RESULT 12		ä .
T31102 filamentous	s hemagglutinin 1 - Haemophilus ducreyi	8
C;Species: C;Date: 22-	Haemophilus ducreyi -Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999	ä
C; Accession R; Ward, C.F	n: T31102 C.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.	6
J. Bacteric A;Title: Ha A:Reference	Bacteriol. 180, 6013-6022, 1998 Title: Heemophilus ducreyi secretes a filamentous hemagglutinin-like protein. Reference number: 230844 MITD:09030726. DMTD:0811662	ដ
A; Accession: A; Status: pro	A,Accession: T31102 A,Etatus: preliminary; translated from GB/EMBL/DDBJ A.Molecule tyre: DNA	E 80 7
A, Residues:	1-4152 <war></war>	ฉียั

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S68218
botulinum neurotoxin type A, nontoxic/nonhemagglutinating - Clostridium botulinum (stra
C;Species: Clostridium botulinum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASN-----SNKIRLEKGRLY 114
                                                                                                                                                                                                                                                                           115 QIKIQY---QRENPTEKGLDFKLYWTDSQNKKEVISSD------NLQLPELKQKSS 161
                                                                                                                                                                                                                                                                                                                                                                  265 INGLSHFBVVARNIDQKG---KITVAKTENQKSVNPANITFAAGSLNYNLKTREATPISS 321
                                                                                                                                                                                                                                                                                                                                                                                                                          162 NSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVD----VKNKRTFLSPWISNIHEKKGLT 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 KYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 SLKELYAK-------KDIDILAKDIELFEKGGLQANNKIILNSTGKINLRNASEV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278 STONTDSETRIIS-KNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDH 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426 SADNVNVKSENLALENASMSANSLDVIVTKIEVNRS----SKVSAGTANIKASNITLDG 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 337 SLSLAGERTW-----ABTWGLNTADTARLW----ANIRYW--T 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        370 GTAPIYNVLPTTSLVLGK------NQTLA-----TIKADENQ-LSQILAPNN-- 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 GEA-----SLVAEKLDINAIDKITNNGTIAGLTANITTKALENRDNALILAHQNLN 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 -----YY------PSKNLAPIALNAQKDFSS------TPITMNYNQFLELEKTKQL 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 FTVNGSHYVNKGDIVSKDKAIVTFSNNSDFTSNGSKLVDAQNNLTVNVNNFNITQGSEII 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       449 RLDTDQVYGNI---ATYNFEN-GRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVER- 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   652 -----LHGNVTLNAKGNFTNSGNLTTMKELNISNIESFI----NÄGNLTTGKNLEVHSNT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 ------RIAAVNPSDPLETTKPDMTL-KEALKIAFG---FNEPNGNLQYQGKDITEF 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703 TVKNDGKLVSIENLNISSKTDFTNNGTLLGLEALKIASGGNFTNASNGSLA-SNKSLDIY 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   659 RYDMLNISSL-RQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTS 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 NNKVYNIGEIYSQAGNISVEAKLILHNDVKL-----SGNITTTK-----SGNATVK 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 DFNF-DQQTSQNIKNQLAELNATNIYTVLDK--IKLNAKMILIRDKRFHYDRNNIAVGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-ESVVKEAHREVINSST----EGLLL----NIDKDIRKILSGYIVEIEDTEGLKEVIND 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         817 DLLNITSOAN--IINKNLLAGGOGLNLTAKGNITNDSNSTAIAVLHSNNDIN----LNA 869
                                                                                                                                                    10 NESESSSØGLLGYYFSDLNFQ-APMVTSSTTGD-----LSIPSSELENIPSENQYF 60
                                                               Query Match
Query Match
Query Score 181; DB 2; Length 4152;
Best Local Similarity 22.2%; Perci No. 1.4;
Matches 187; Conservative 118; Mismatches 321; Indels 218;
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C;Genetics:
A;Gene: lspAl
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hypothetical protein yqfG [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Species: Lactococcus lactis subsp. lactis c;Date: 23.4mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C;Accession: A86827
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl Aschoutin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrl A;Tile: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s: A;Reference number: A86625; MUID:21235186; PMID:11337471 A;Status: Perliminary A;Molecule type: DNA A;Status: Perliminary A;Status: Perliminary A;Residues: 1-1072 <STO> A;Cross-references: GB:AE005176; PID:g12724625; PIDN:AAK05715.1; GSPDB:GN00146 A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                     969 SVDRLKRQLLIFIDDNLVANRSIKEILNIYSSNIISLLSENNPSYIEGLTILNKPTTS-Q 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 158 QKSSNSRKKRSTSAGPTVPDRDNDGI----PDSLEVEGYTVDVKNKRTFLSPWISNIHEK 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 EASTNSNSISLSPSNISSTSVLESTISSSNFSNVABVANNSLASVNNSSSSVLSSTSTA 594
                                                                                                             909 RNLGKDTIKSKLIGSKEDNCGWEIYFQDTGLVFNMIDSNGNEKNIYLSDVSNNSWHYITI 968
                                                                                                                                                                                    599 --DR--NNIAVGADESVV-KEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLK 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 VEÇVDVASSESTQDANSASLYPISEASSVTDNTLNSISSLDSSISSSQTENSQSGASSTA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 TNILPPSNPTESNSVSDÓTSSEASTNSNSSISLSPSNISSTSDSESATNSSDFSNVAEVA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 KGLTKYKS----SPEKWS-----TASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPI 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 VHVDM----ENI-----ILSKNEDQSTQNTDSETRIISKNTSTSRTHISEVH 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 GNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSL--AGERTWAETWGLNTADTARLNA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNQ----SNSSEATKVDNNSST----HSSNILNSGSNDSSDSDSDSDSSNL-- 699
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                                                                                                                                                                                                                                                                                                                           EVINDRYDMLNISSLRODGKTFIDFKKYNDKLPLYISNPNYKVN---VYAVTKENTI--- 707
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4.8%; Score 179.5; DB 2; Length 1072;
Best Local Similarity 19.4%; Pred. No. 0.22;
Matches 160; Conservative 142; Mismatches 342; Indels 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 INNTHNLNLQASKFKLLSINPNKQY 1105
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                                                    --LDKIKLNAKM----
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A Mesidues: 1-13,145-155 <FUL>
A Mesidues: 1-13,145-155 <FUL>
A SExperimental source: strain NIH
C Genetics:
A Senerics:
C Seperfault: tetanus toxin
C Superfault: tetanus toxin
C Superfault: botulinum neurotoxin type A, nontoxic/nonhemagglutinating #status expe
A, Variety: strain NIH
C, Cate: 15-Reb-1997 #sequence_revision 13-Mar-1997 #text_change 02-Jun-2003
C, Accession: 568218, 574301
C, Accession: 568218, 574301
R, Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.
ERBS Lett. 376, 41-44, 1995
A, Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components
A, Reference number: 567988; MUD: 96096783; PMID: 8521962
A, Accession: 5689
A, Molecula type: DNA
A, Residues: 1-1193 - FUJ
A, Residues: 1-1193 - FUJ
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4.8%; Score 180; DB 2; Length 11:
Best Local Similarity 19.6%; Pred. No. 0.24;
Matches 181; Conservative 131; Mismatches 319; Indels
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EVHGNAEVHA-----SFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLN
                                                      TVD-VKYGGNIAYDGV-TRPVBKTIBS-----GK-----KLDVGGVIENVG-----
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Job time : 16.0855 secs
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: A10452
E;Accession: A10452
E;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Apparkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. Apparkhill, J.; Wren, B.W.; Chillingworth, T.; Cronin, A.; Stevens, R.M.; Davies, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Reference number: AB0001; MUD:21470413; PMID:11586360
A;Accession: A10452
A;Status: preliminary
A;Molecule type: DNA
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4.7%; Score 179; DB 2; Length 1635;
Best Local Similarity 19.4%; Pred. No. 0.44;
Matches 176; Conservative 137; Mismatches 315; Indels 278;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Run on: May 3, 2004, 19:27:02 ; Search time 8.2539 Seconds (without alignments).
4636.784 Million cell updates/sec
Title: US-09-848-909A-10
Perfect score: 3774
Sequence: I EVWQENRLLNESESSSQGLL.....TSTNGIKKILIFSKKGYEIG 735

Sequence: 1 EVKQENRLINESESSSQGLL.. Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Dacilius	P13422 bacillus an	P04932 plasmodium	P04933 plasmodium	Q03661 saccharomyc					P08799 dictyosteli	Q10411 schizosacch	P41508 mycoplasma	P19321 clostridium	Q00798 plasmodium	O13735 schizosacch	Q9zlt1 helicobacte	Q00799 plasmodium	P97434 mus musculu								ď		P34487 caenorhabdi	P75109 mycoplasma	ω	968 sacc	0496 clostridi	₹#
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## ALIGNMENTS

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MUTAGENESIS OF LYS-426; ASP-454 AND PHE-456
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CO2 and
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It is a cativation by furin or a furin-like protease cleaves the protein. The two barts, PA-63 the latter is the mature protein. The cleavage occurs at the cell surface and probably in the serum of infected animals as well; both native and cleaved PA are able to bind to the cell receptor. The release of PA20 from the remaining receptor-bound PA63 exposes the binding site for EF and LF, and promotes oligomerization and internalization of the protein.

MISCELLANGOUS: In Ref.9 multiple mutagenessis experiments were performed that the residues present in the small loop of domain 4, and not the ones in the large loop, are involved in
                                                                                                                                                                                                                                                                                                                          MEDILINE-97192099; PubMed=9039918;
Petosa C., Collier R.J., Klimpel K.R., Leppla S.H., Liddington R.C.;
"Crystal structure of the anthrax toxin protective antigen.";
                                                                                                                                                                                                 Chauhan V., Bhatnagar R.;
"Identification of amino acid residues of anthrax protective antigen involved in binding with lethal factor.";
Infect. Immun. 70:4477-4484 (2002).
                                                                                                                       LEU-216; PHE-231; LEU-232; PRO-234; ILE-236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACTERIAL BINARY TOXIN FAMILY
                                         antigen that block
MEDINE-21269403; Pubmed-1113126;
Sellman B.R., Nassi S., Collier R.J.;
"Point mutations in anthrax protective
                                                                                                                                                                                                                                                                                                           (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21428689; PubMed=11544370;
                                                                                  Biol. Chem. 276:8371-8376(2001)
                                                                                                                                                                                    MEDLINE=22112896; PubMed=12117959;
                                                                                                   MUTAGENESIS OF PRO-213; LEU-2
LLE-239; TRP-255 AND PHE-265.
STRAIN-Sterne;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                         Nature 385:833-838(1997)
                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY
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                                                                   translocation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --GLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPN 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 KKPSNHLTNSPVIITLAGKDSGVGELYRVLS-----DGTGFLDFNKFDENWRSLV-DPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 MNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface antigens)
                                                                                                                                                              MEDILINE=59445483; PubMed=10515943; MEDILINE=59445483; PubMed=10515943; Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K., Keim P., Kochler T. M., Lamke G., Kumano S., Mahillon J., Manter D Martinez Y., Ricke D., Svensson R., Jackson P.J.; "Sequence and organization of pXO1, the large Bacillus anthracis plasmid harboring the Anthrax toxin genes."; J. Bacteriol. 181:6509-6515(1999).
MEDLINE=89172073; PubMed=3148491;
Melkos S.L., Lowe J.R., Eden-Mccutchan F., Vodkin M., Leppla S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T -> A (IN REF. 1).
KSCNCILIYVEVSQLMNSVFY -> NHVIVYLSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 235.5; DB 1; Length 204; 34.6%; Pred. No. 2.6e-05; iive 36; Mismatches 47; Indels 23;
                                                          the DNA encoding protective antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-86136024; PubMed=3004972;
Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa
Stunnenberg H., Bujard H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                694 YKVNVYAVTKEN-TIINPSENGDTSTNGIKKILIFSKKGYEI 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 AA; 23029 MW; E1657B23AE4273FD CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite (PMMSA) (P190)
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                                                            of,
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93
204
                                                        Sequence and analysis
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TRANSMEM 162 182
CONFLICT 93 93
CONFLICT 184 204
                                                                                  Bacillus anthracis.";
Gene 69:287-300(1988)
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P04932;
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Best Local
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MSP1_PLAFK
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 NANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIA 449
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                                                                                                                               EVKQENRILINESESSSQGILGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYF
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                                                                                                                                                                                                                                                  QRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDN
                                                                                                   EVKQENRLINESESSSQGLLGYYFSDLNFQAPMVTSSTTGDLSIPSSELENIPSENQYF
                                                                  Gaps
                                                                ö
                               Length 764;
                                                                2; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                           Score 3758; DB 1;
Pred. No. 1.2e-177;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13422; 093377;
01-JAN-1990 (Rel. 13, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein px01-111.
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                                              al Similarity 99.6
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NSNSSTVAIDHSLSLAGERTWAETWGLNTADTARLNANIRYVNTGTAPIYNVLPTT---- 381
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                                                                                                                -SLVLGKNOTLATIKADENQLSQILAPNNYYPSKNLAPIA---LNAQKDFSSTPITMNYN
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Holder A.A., Lockyer M.J., Odink K.G., Sandhu J.S., Riveros-Moreno
Nicholls S.C., Hillman Y., Davey L.S., Tizard M.L.V., Schwarz R.T.,
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Submitted (MAR-1991) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
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1-FEB-1996 (Rel. 33, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Merozoite surface protein 1 precursor (Merozoite surface antigens)
(PPMSA) (P195).
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kDa and 19 kDa antigens which are the major surface antigens
merozoites. The maturation take place during schizont.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure of the precursor to the three major surface antigens of Plasmodium falciparum merozoites.";
Nature 317:270-273(1985).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5848;
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                                                                                                                                                                                                                                                        (Potential).
PTM: Merozoite surface antigen contain the sequence of 83 kDa, 4
kDa and 19 kDa antigens which are the major surface antigens of
merozoites. The maturation take place during schizont.
                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
              "Polymorphism of the precursor for the major surface antigens of plasmodium falciparum merozoites: studies at the genetic level."; EMBO J. 4:3823-3829(1985).
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InterPro; IRP006209; EGF_like.
Pfam; PF000008; EGF; Prolyprotein; Repeat; Signal; Glycoprotein;
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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REPEAT.
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                                                                                                                                                      Tolle R., Bujard H.;
ed (JUN-1995) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 0.12;
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                                                                                                                                  SEQUENCE FROM N.A.
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Best Local Simil
Matches 170;
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Submitted
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                          1466 IQDKLADFKKNNNFVGIADLSTDYNHNNLLTKFLSTGMVFBNLAKTVLSNLLDGNLQG-M 1524
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577 VLDKIKLNAKMN--ILIRDKRFHYDRNN-----IAVG-ADESVVKEAHREVINSSTEGLL
                                                                                                                   ------REECKCLLNYKQEGDKC-
                                                                              LNIDKD--IRKILSGYIVBIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=S288c / AB972;

MEDLINE=37313268; PubMed=9169872;

Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,

Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,

Cagels K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.

Rice P., Skelton J., Walsh S., Whitchead S., Barrell B.G.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 278; Indels 280;
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18.4%; Pred. No. 0.46;
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GO; GO:0005634; C:nucleus; IDA.
GO; GO:0006348; P:chromatin silencing at telomere; IMP.
                                                                                                                                                                                                                                                                                                           1658 AA
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                                                                                                                                                                                                                                                                                                           STANDARD;
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S05603; S05603
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                                         GYTVDVKNKRIFL---SPWISNIHE--KKGLTKYKSS----PEKWSTASD----- 231
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Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Structural maintenance of chromosome 3 (DA-box protein SMC3)
SMC3 OR VJL074C OR J1049.
Saccharomyces cerevisiae (Baker's yeast).
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MEDLINE=96208490; PubMed=8641269;
Galibert F., Alexandraki D., Baur A., Boles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1230 AA.
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EMBL; Z49349; CAA89366.1; -.
EMBL; X88851; CAA61313.1; -.
PIR; S56850; S56850.
GermOnline; 141688; -.
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            GG; GO:0007151; P: Sporulation (sensu Saccharomyces); IMP.
GG; GO:0007151; P: Sporulation (complex formation; IMP.
InterPro; IPR003495; ABC_transporter.
InterPro; IPR003495; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PP02463; SMC_N: 1.
Mitosis; Cell cycle; Chromosome partition; ATP-binding; Coiled coil; Nuclear protein.
Nuclear protein.
Nu BIND
32
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172
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COILED COIL (POTENTIAL).
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ALA/ASP-RICH (DA-BOX).
MW, B152D88F7780341F CRC64;
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4.5%; Score 169.5; DB 1; Length 1
Best Local Similarity 19.8%; Pred. No. 0.51;
Matches 182; Conservative 136; Mismatches 355; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | SECTION OF PROM N.A.
bMed=8686379; PubMed=8686379; PubMed=8686379; PubMed N. Hagiwara H., Ozawa M., Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
| Sasanuma M., Tsuchiya Y., Shibata T., Hanaoka F., Murakami Y.;
| Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome VI from Saccharomyces cerevisiae.";
| Yeast 12:149-167(1996):
| FUNCTION: Associates with the SIT4 phosphatase in a cell cycle dependent manner. May be directly or indirectly involved in SIT4-dependent functions in budding and in normal Gl cyclin
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=96220458; PubMed=8649382;
Luke M.M., della Seta F., di Como C.J., Sugimoto H., Kobayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 98-1000 FROM N.A.
SEQUENCE OF 98-1000 FROM N.A.
STRAIN-S288C / AB972;
MUTAKAN-S2880029; PubMed=7670463;
MUTAKANI Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama Yamazaki M., Tashiro H., Eki T.;
"Analysis of the nucleotide sequence of chromosome VI from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIM: Hyperphosphorylated in the absence of SIT4. SIMILARITY: Belongs to the SAPS family.
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01-OTT-1996 (Rel. 34, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
SAP155 OR YFR040W.
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Mol. Cell. Biol. 16:2744-2755(1996).
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Nat. Genet. 10:261-268(1995).
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4.4%; Score 166; DB 1; Length 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNSGGANYGFYCH-INGNGKEYWKKLIS-----SANSANKPYIEVTYIIPKGN 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     326 NSNSSTVAIDH--SLSLAGERTWAETMGLNTADTA------RLNANIRYVNTGTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            719 GAKRNYSFKIIAYNKDGEAIASPAATPALPDIARPKNVTGYLYTNTKSSOTGYVNLIWEK 778
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2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;
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                        SEQUENCE
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( InterPro; IPR00530; YL.)

R InterPro; IPR00530; YL.)

DR Appro18; CBM 4 9; 1.

DR TGRFMS; TGR01643; Y_repeat; 14.

DR TGRFMS; TGR01643; Y_repeat 2x; 17.

CG11 wall; Repeat; Signal; Complete proteome.

FT CHAIN 29 2334 WALL-ASSOCIATED PROTEIN.

FT CHAIN 504 869 3 X 101 AA APPROXIMATE TANDEM REPEATS.

FT REPEAT 504 605 1-1.

FT REPEAT 504 605 1-2.

FT REPEAT 504 605 1-2.

TG9 869 1-3.

TG9 869 31 X 21 AA APPROXIMATE TANDEM REPEATS OF X (4) - G-X (4) - [YF] - X-D-X (2) -G-X (4).
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                    -i- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM, MOTILITY, SECRETION OR DIFFERENTIATION.
-!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED INTO THE MEDIUM.
                                                                                                                                                                           -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED MOTIF REPEATED 31 TIMES.
-!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME SIMILARITY TO THE REPEATED IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
  complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (APPROXIMATE)
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2-18.
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EMBL; D31856; BAA06656.1; -...
EMBL; D29985; BAA06560.1; -...
EMBL; D33026; BAA1683.1; -...
EMBL; Z99124; CAB15959.1; -...
SA2920; S32920.
Subtilist; BG10797; wapA.
INTERPRO; IPR003305; CBM_
                                   subtilis.";
Nature 390:249-256(1997)
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Fisher A.J., Smith C.A., Thoden J.B., Smith R., Sutoh K., Holden H.M.
1574 QQLL------GELNYV-RHKCRYDIEFAVKKVARLVNYPHERVFYMIYKIIQYL--
                                                                                                                                                                                                                                                                                                                  584 NAKWNILIRDKRFHYDRN----NIAVGADESVVKEAHRE----VI-----NS
                                                          429 STPITMNYNQFL-ELEKTKQLR-----LDTDQVYGNIATYNFENGRV-----
                                                                                                                                              RVDTGSNWSEVLPQ1QETTAR11FNGKDLNLVERRIAAVNP-SDPLETTKPD-----MTL
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MEDLINE-88112226; PubMed=2828113;
MEDLINE-88112226; PubMed=2828113;
Magle G., Noegel A., Scheel J., Gerisch G.;
Phosphorylation of threonine residues on cloned fragments of Dicryostelium myosin heavy chain.";
FERS Lett. 227:71-75(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SECUENCE FROM N.A. MEDLINE=87092266; PubMed=3540939; Martick H.M., de Lozanne A., Leinwand L.A., Spudich J.A.; Warrick H.M., de Lozanne A., Leinwand L.A., Spudich J.A.; Dictyostellum discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MX2;
MEDLINE-90353583; PubMed-2287408;
Lucck-Vielmeter D., Schleicher M., Grabatin B., Wippler J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBL_TaxID=44689;
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01-OCT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Myosin II heavy chain, non muscle.
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STRAIN=S2862 / FY1679;
STRAIN=S28862 / FY1679;
STRAIN=S28862 / FY1679;
MEDLINE=97103775; PubMed=8948101;
Cziepluch C., Kordes E., Pujol A., Jauniaux J.-C.;
"Sequencing analysis of a 40.2 kb fragment of yeast chromosome X "reveals 19 open reading frames including URA2 (5' end), TRK1, PB82, SPT10, GCD14, RPB1, PH086, NCA3, ASF1, CCT7, GZF3, two tRNA genes, three remnant delta elements and a Ty4 transposon.";
                                                                                                                                                                                                    Saccharomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00665; rve; 1.
SMART; SM0343; ZnF C2HC; 1.
Transposable element; Hypothetical protein.
SEQUENCE 1803 AA; 207693 MW; 16DCD7284A8D52D3 CRC64;
                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
                                               747024; P87192;
01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Transposon Ty4 207.7 kDa hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.3%; Score 164; DB 19.5%; Pred. No. 1.6;
                                 1803 AA
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                                                                                                                                       Transposon Ty4 207.7 kDa l
TY4B OR YJLI13W OR J0780.
                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.

MEDLINE=98070605; PubMed=9405148;

Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

C. f. Argy crystal structure and solution filucrescence characterization of mystellium discoideum myosin motor domain.";

Dictyostellium discoideum myosin motor domain.";

J. Mol. Biol. 274:394-407(1997).

J. Mol. Biol. 274:394-407(1997).

C. i- FUNCTION: Myosin is a protein that binds to actin and has ATPase activity that is activated by actin.

C. i- SUBUNIT: Myosin II heavy chain is two-headed. It self-assembles into filaments. Hexamer of 2 heavy chain subunits (MHC), 2 alkali ilght chain subunits (MLC) and 2 regulatory light chain subunits (MLC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ...-:- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE POSTERIOR CELL
                                                                                                                                                                                                                                                                                           X.TAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 1-762.
MEDLINE=97452580; PubMed=9305951;
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP complexes of the Dicryostellum discondeum myosin motor domain.";
Biochemistry 36:11619-11628(1997).
                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-762.
MEDLINE-S6206189; PubMed=8611530;
Smith C.A., Rayment I.;
"X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostellum discoideum myosin motor domain to 1.9-A resolution.";
[7]
MEDLINE-95345067; PubMed-7619796; Smith C.A., Rayment I.; "X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated had of Dictyostelium discoideum myosin to 2.7-A
                                                                                                            Biochemistry 34:8973-8981(1995).
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1MMA, 03-DEC-97.

1MMD; 17-AUG-96.

1MMN; 03-DEC-97.

1MND; 17-AUG-96.

1MND; 17-AUG-96.

1UND; 23-DEC-96.

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ilarity 19.4%; Pred. No. 2.3;
Conservative 113; Mismatches 219;
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KA WEDLINE-21848401; PubMed=11859360;

KA WOOd V., Gwilliam R., Hajandream M.A., Lyne M., Lyne R., Stewart A., Sagouros J., Peat N., Hayles J., Basham D., Bowman S., A Brooks M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gollins M., Connor R., Huckle E.J., Hunt S., Jageln G., A., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jageln K., A., Marphy L., Miblett D., Odell C., A., Monosy P., Noule S., Mungall K., Murphy L., Miblett D., Odell C., R., Rutherford K., Rutter S., Saunders D., Gaeger K., Sharp S., R., Rutherford K., Taylor R.G., Taverson D., Quall M.A., Rabbinowitsch E., R., Redlton U., Simmonid M., Squares R., Squares S., Stevens K., Whitehead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Beger P., Zimmermann W., Wedler M., Schner K., Hurst S.M., Gabel C., Fuchs M., Fritzc C., Holzer E., Mooetl D., Hilbert H., Rabinert F., Pores S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., A., Daga R.R., Cruzado L., Jimenez J., Sanchez M., Gelzon A., Thode G., Boniquez A., Revuelta J., Moreno S., Almstrong J., Porsburg S.L., Doentutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J., R., The Gronne sequence of Schizosaccharomyces pombe.";
R. Whire Alf. S71-RR. The R. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR. Marine Alf. S71-RR.
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION. MEDLINE=20107136; PubMed=10639340; Ikemoto S., Nakamura T., Kubo M., Shimoda C.; Nakamura T., Kubo M., Shimoda C.; Sombe sporulation-specific coiled-coil protein Spol5p is loc to the spindle pole body and essential for its modification."; J. Cell Sci. 113:545-554 (2000).
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Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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COILED COIL (POTENTIAL)
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-!- SUBCELLULAR LOCATION: Spindle pole body.
-!- SIMILARITY: Belongs to the MPC70 family.
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EMBL; AB027811; BAA87115.1; -.
PIN; T38077; T38077; GeneDB_SPombe; SPACIF3.06c; -.
Sportlation; Colled coil.
DOMAIN 804 1235 COIL
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                                                                                                                                                      Schizosaccharomyces.
NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                    LENIPSENQYFQSAIWS---GFIKV-----KKSDEYTFATSADNHVTWWVDDQEVINKAS 101
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Matches 177; Conservative 132; Mismatches 328; Indels 232;
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1481 1723 COILED COIL (POTENTIAL).
1957 AA; 222785 MW; 3F480CA06171D9DA CRC64;
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P115 MYCHR
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276 ---FKTEVE-----SSIQEITSKLDNLKNALSEINLQEARIEERRKLIISGEIV-V 322
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                                                                                                                                                                                                                                                                               -!- SUBCELLUAR LOCATION: Cytoplasmic.
-!- DOWAIN: Consists of two putative central coiled-coil regions
-!- DOWAIN: Consists of two putative globular regions at the N- and C-termini.
-!- SIMILARITY: BELONGS TO THE SMC PAMILY. SIMILAR TO OTHER MYCOPLASMA
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; Mismatches 342; Indels 277;
                                                                     Mycoplasma hyorhinis.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBI_TaxID=2100;
                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=91138990; PubMed=1825306;
Notarnicola S.M., McIntosh M.A., Wise K.S.;
"A Mycoplasma hyorhinis protein with sequence similarities to nucleotide-binding enzymes.";
Gene 97:77-85(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 161.5; DB 1; Length 979;
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231 400 COILED COIL (POTENTIAL).
569 821 COILED COIL (POTENTIAL).
884 912 ALA/ASP-RICH (DA-BOX).
979 AA, 110566 MW; 30D51CS6B56280F4 CRC64;
01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR003493; ABC transporter.
InterPro; IPR005289; GTP-bindding_dom.
InterPro; IPR003405; SMC_C.
InterPro; IPR003995; SMC_N.
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Pfam; PF02463; SMC_M; 1.
TIGRFAMS; TIGRO0650; MG42; 2.
ATP-binding; Coiled coil.
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--SEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAE---TMGLNTA 355
                 383 KKSAAAANINILKQQFENKSFLSKGIKTIKDNSFLFDGYIGLASELFKVESEFSLAIETV 442
                                                                           387 KNOTLATIKADENO----LSQILAPNNYYPSKNLAPI------ALN 422
                                                                                         AQKDFSSTPITMNYNQFLELEKTKQLRLDTDQ------VYGNIATYNFENGRVRVD 472
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                                                                                                                                                          473 TGS------508 TGS-----508 TGS------ 508
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MEDLINE=93042276; PubMed=1420572;
Sunagawa H., Ohyama T., Watanabe T., Inoue K.,;
Sunagawa H., Ohyama T., Watanabe T.,
The complete amino acid sequence of the Clostridium botulinum type neurotoxin, deduced by nucleotide sequence analysis of the encoding phage d-16 phi genome.";
J. Vet. Med. Sci. 54:905-913(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clostridium botulinum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BVD/-3;
MEDLINE=91016853; PubMed=2216736;
Binz T., Kurazono H., Popoff M.R., Eklund M.W., Sakaguchi G.,
Kozaki S., Krieglstein K., Henschen A., Gill D.M., Niemann H.;
"Nucleotide sequence of the gene encoding Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BONT/D)
                                       --ANIRYVNTGTAPIYNVLPTTSL-
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Nucleic Acids Res. 18:5556-5556(1990).
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Reticulocyte binding protein 1 precursor
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hes 146;
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                                                                                SIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNS
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TIPSSWISNI---DKY---KKIFSEKYNFDKDNTGNFVVNIDKFNSLYSDLTNVMSEVVYS
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                                                                224;
                                              DB 1; Length 1276;
                                                              Conservative 117; Mismatches 291; Indels
K -> N (IN STRAIN CB16).
N -> K (IN STRAIN CB16).
Q -> R (IN STRAIN CB16).
MW; C1ECSOF46C8233E2 CRC64;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 69:1213-1226(1992).
-!- FUNCTION: Involved in reticulocyte adhesion. Specifically binds human reticulocyte cells.
-!- SUBDNIT: Homodimer (Potential).
-!- SUBCELLUIAR LOCATION: Membrane-bound.
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=31273;
                                                                                                                                                                                                                                            MEDLINE-92315338, PubMed-1617731,
Galinski M.R., Medina C.C., Ingravallo P., Barnwell J.W.;
"A reticulocyte-binding protein complex of Plasmodium vivax
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RETICULOCYTE BINDING PHEXTRACELLULAR.

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2; Mismatches 297;
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regulator Aip3p/Mol. Biol. Cell	Pfam, PP03915; P Coiled coil; Cyt DOMAIN 1009 SEQUENCE 1385 Query Match Best Local Similari Matches 147; Cons	26 DLN 326 DRK 75 DEY 384 NVF	105 KIRLEKG     :  440 PILLPRG	144 EVI   ::   500 ELLERQI   188 EVEGYTV			364 IRYUN 	754 NVSGSPS 478 SEVLPOI :   :: 812 ANELGEL	
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nservative 125; Mismatches 293; Indels 202; Gaps
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        955 KFYQQVKNNQ---LELASLKQISAAFFRRIPLKIKDFKKEINAFNEK 998

        Search completed: May 3, 2004, 19:36:55

        Job time: 12.2539 secs
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